```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

- protein search, using sw model OM protein July 11, 2002, 10:50:47; Search time 16.34 Seconds (without alignments) 470.450 Million cell updates/sec Run on:

1 ADKYKTFEAAFTVSSKRNLA.....SEALHIIAGTPEVHAVKPGA US-09-696-169A-18 409 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

283138 seqs, 96089334 residues Searched: 25992 Total number

of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 80

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		hypothetical prote	ب	hypothetical prote	hypothetical prote	_				vitellogenin Al -	hypothetical prote	probable lipoprote	hypothetical prote	ubiquinolcytochr	andropin precursor	protein gp50 - pha	hypothetical prote	hypothetical prote	30S ribosomal prot	3,5-dichlorocatech	hemoglobin alpha-2	hypothetical prote	anion exchanger 3	hypothetical prote	phosphoprotein pho	hypothetical prote	al	_	leukotriene-A4 hyd
SUMMARIES	QI	AI2346	T49967	T41731	D86945	F82545	T13184	H82699	B33488	AE3538	A23876	D82775	B81354	E82438	A53768	S13450	T13137	A23697	T06833	C86842	S32316	E60515	F82739	I38497	18	2	32	E83671	YYFIS	S70651
	DB	7	7	C)	7	7	~1	7	7	~1	~1	7	7	7	7	7	~	~	7	7	7	7	~	7	7	~	~	7	П	7
	Length	68	75	77	79	54	49	26	61	9	71	74	75	09	17	57	73	75	77	17	44	09	9	72	63	64	78	79	36	49
oжР	Query Match							10.8										10.4		10.4										
	Score	46.5	46	46	46	45.5	45	44	44		έ,	ά,	٠	43	43	42.5	ς.	42.5	42.5	42.5	₹	41.5	41	41	0	0	40.5		40	
	Result No.	н	2	m	4	S	9	7	8	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote	hypothetical prote	unknown protein en	osteocalcin - emu	hypothetical prote	RP511 protein homo	hypothetical prote	M-like protein enn	hypothetical prote	ribosomal protein	hypothetical prote	hypothetical prote	ribosomal protein	hypothetical prote	hypothetical prote	
AI2213	A97900	C85714	S02208	AD3257	F97781	AB3540	S61801	S52358	R3KM72	E84079	A82732	T45363	C71652	AD2576	E64159
7	7	~	7	7	7	7	7	7	_	7	7	7	7	7	7
64	65	97	48	9	70	72	80	43	52	26	57	61	64	89	72
æ	ω.	8.6	9.7	9.7	9.7	9.7	9.7	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5
9.	9	•													
	40		39.5	39.5	39.5	39.5	39.5	39	39	39	39	39	39	39	39

#### ALIGNMENTS

Appenhetical protein as14328 [imported] - Anabaena sp. (strain PCC 7120)
C; Species: Anabaena sp.
A; Note: Anabaena sp.
A; Note: Anabaena sp.
C; Strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
C; Dates: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 11-Jan-2002
C; Accession: A1346
R; Kaneko, T; Nakamura, Y; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Natanabe, A.; Irigu
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Res. 8, 205-213, 2001
A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A; Reference number: AB1807; MUID:21595285; PMID:11759840
A; Accession: A12346
A; Accession: A12346
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-68 «KUR>
A; Residues: 1-68 «KUR>
A; Cross-references: GB:BA000019; PIDN:BAB76027.1; PID:g17133464; GSPDB:GN00179
C; Genetics:

A; Gene: as14328

Gaps ; Length 68; Indels ch 11.4%; Score 46.5; DB 2; Similarity 28.3%; Pred. No. 2.7e+02; 13; Conservative 7; Mismatches 25; Query Match Best Local Similarity Matches

ij

# 17 RNLADAVSKAPQLVPKLDEVYNAAYNAADHAAPEDKYEAFVLHFSE 62 δŏ

| | : :| |: | |: | |: | 8 RQLVEKALDIKKLTPEIENEINVELTAMGHISDVD-YEALELLMAE 52 Op

### RESULT

T49967

Pypothetical protein FBM21.210 - Arabidopsis thaliana (5.5pecies: Arabidopsis thaliana (mouse-ear cress) (5.5pecies: Arabidopsis thaliana (mouse-ear cress) (5.5pecies: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 02-Jun-2000 (5.5Accession: T49967 (7.5 #dley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, A.; Reference number: 224493 A.; Reference number: 224493

s.;

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-75 <BEV>

A;Cross-references: EMBL:AL353993; GSPDB:GN00063; ATSP:FBM21.210 A;Experimental source: cultivar Columbia; BAC clone F8M21

C;Genetics: A;Gene: ATSP:F8M21.210

A; Map position: 5 A; Introns: 16/3; 38/3

Thu Jul 11 11:40:39 2002

```
C;Dates 18-Aug-2000 #Sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C;Accession: P82545
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq Nature 406, 151-157, 2000
A;Tille: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717
A;Notecession: R62545
A;Status: preliminary
A;Notecession: R62545
A;Status: preliminary
A;Residues: 1.54 <SIMA
A;Residues: 1.54 <SIMA
A;Residues: 1.54 <SIMA
A;Cross-references: GB:AE004060; GB:AE003849; NID:g9107735; PIDN:AAF85327.1; GSPDB:GN
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Carraro, D.M.; Carrer
Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Frenca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Remper, E.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, E.B.; La
chado, M.A.; Madeira, A.M.; Madeira, H.M.F.; Marino, C.L.; Marques, M.A.; Madeira, A.M.; Madeira, M.A.; Gensan, A.J.; Marcues, B.C.; Palmieri,
Rodrigues, V.; Rosa, A.J.; de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa
A;Authors: Ga Silva, A.B.; de Silva, F.M.; Silva, A.M.; Silva Jr., W.A.; de Silva
A;Reference number: A59328
A;Contents: annotation
A;Contents: annotation
A;Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein R49 - Lactobacillus phage phi-gle
C;Species: Lactobacillus phage phi-gle
C;Species: Lactobacillus phage phi-gle
C;Species: Lactobacillus phage phi-gle
C;Date: 13-Aug-1999 #sequence_revision i3-Aug-1999 #text_change 13-Aug-1999
C;Accession: T13184
R;Kodaira, K.I.; Oki, M.; Kakikawa, M.; Watanabe, N.; Hirakawa, M.; Yamada, K.; Taket
Gene 187, 45-53, 1997
A;Title: Genome structure of the Lactobacillus temperate phage phi gle: the whole gen
A;Reference number: 217631; MUID:97225795
A;Accession: T13184
A;Reference number: 217631; MUID:97225795
A;Accession: T13184
A;Reference number: 217631; MID:9912136; PID:e247135; PIDN:CAA66760.1
C;Genetics:
A;Note: Rorf49
                                                                   hypothetical protein XF2529 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.0%; Score 45; DB 2; Length 49; 25.5%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEEHETYSATQVSQSVTNLVVEIANNPKTKKSPAMVAALAELLEALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ADKYKTFEAAFTVSSKRNLADAVS-----KAPQLVPKLDEVYNAAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 NNPSNEKHHTTPPLELSDECVSNFSELIKALAAYKEINAKKKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38 NAAYNAADHAAPE-DKYEAFVLHFSEALHIIAGTPEVHAVKPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45.5; DB 2;
Pred. No. 2.7e+02;
7; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.1%;
30.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 11.1%
Best Local Similarity 30.2%
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 25.5
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Öλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P.R.; Hc
Holroyd,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           So
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R. Cole, S.T.; Eighmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; F. B.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroydeam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A.Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S. Airiter manner: A86909; MuID:21128732; PMID:11234002
A.Accession: D86945
A.Steference number: A86909; MuID:21128732; PMID:11234002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-77 <LIN>
A;Cross-references: EMBL:AL023781; PIDN:CAA19343.1; GSPDB:GN00068; SPDB:SPCC338.12
A;Experimental source: strain 972h-; cosmid c338
                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AL450380; NID:913092614; PIDN:CAC29800.1; GSPDB:GN00147 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ö.
                                                                                                                                                                                                                                                                                                                                                            probable proteinase precursor - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: D86945
                                                                                                                                                                                                                                                                                                                                                                                                                                                          C,Accession: T41731
R;Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris,
submitted to the EMBL Data Library, June 1998
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 AFTVSSKRNLADAVSKAPQ-----LVPKLDEVYNAAYN-----AADHAAPEDKYEA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |: :| | : :|: | : :| : | 3 AYGTASGRRILEAILIASDIDIIVYHLLTSKVHQ-YHIAYHEEGNVLAGNHQVVSENY -- 59
                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
          Length 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.2%; Score 46; DB 2; Length 77;
.larity 38.5%; Pred. No. 3.5e+02;
Conservative 4; Mismatches 12; Indels
                                                                          23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Len., 3.7e+02; 25;
                                                                                                                                                                                                   31 NMKLKVLKPPLIIKPLFFLYNKMPKAGGDVSPVSLISSFMIH 72
                                                                                                                                   18 NLADAVSKAPQLVPKLDEVYNAAYNAADHAAPEDKYEAFVLH 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein [imported] · Mycobacterium leprae
          Score 46; DB 2; ]
Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: T41731
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                   8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 46; DB
; Pred. No. 3.7e
14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 YKTFEAAFTVSSKRNLADAVSKAPQL 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37 YDTVFKGFSVSLPENAVDALSAHPEI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----ALHLLASSIDPIPRAKYPG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 FVLHFSEALHIIAGT -- PEVHAVKPG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.2%;
24.4%;
   ch 11.2%;
1 Similarity 26.2%;
11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: Z22013
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: SPDB:SPCC338.12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: ML0292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics:
                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09
                                                                                                                                                                                                qq
                                                                                                                                   ŏλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db
```

;;

Gaps

ij

Gaps

```
C;Accession: AE3538
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melit
A;Reference number: AD3252; PMID:11756688
A;Accession: AE3538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyaccession: A23876

R;Germond, J.E.; Walker, P.; ten Heggeler, B.; Brown-Luedi, M.; de Bony, E.; Wahli, W Nucleic Acids Res. 12, 8595-8609, 1984

A;Title: Evolution of vitellogenin genes: comparative analysis of the nucleotide sequ A; Racerence number: A93543; MUID:85062835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-71 <GES
A;Cross-references: GB:X01168; NID:964500; PIDN:CAA25615.1; PID:964501
A;Note: the authors translated the codon CTT for residue 8 as Ile, and CAA for residu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-74 <SIM>
A; Cross-references: GB:AE003912; GB:AE003849; NID:g9105560; PIDN:AAF83497.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein XF0687 XF2521 [imported] - Xylella fastidiosa (strain 9a5c) C; Species: Xylella fastidiosa (c; Species: Xylella fastidiosa (c; Species: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000 C; Accession: D82775; G82547 G8254 G8254 G8254 G82575; G82575; G82575; G82575 G82575; G82575 G82575; G82575 G825775 G8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-68 <KUR>
A; Cross-references: GB-AE008918; PIDN:AAL53472.1; PID:g17984374; GSPDB:GN00191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Xenopus laevis (African clawed frog)
C;Date: 08-Aug-1987 #sequence_revision 08-Aug-1987 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 LADAVSKAPQLVPKLDEVYNAAYNAADHAAPEDKYEAFVLHFSEALHIIAGTPE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ADKYKTF-EAAFTVSSKRNLADAVSKAPQLVPKLDEVYNAAYNAADHAAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.6%; Score 43.5; DB 2; 27.5%; Pred. No. 5.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43.5; DB 2;
Pred. No. 6.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vitellogenin Al - African clawed frog (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Experimental source: strain 9a5c A, Accession: G82547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 10.6%;
Best Local Similarity 29.6%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Introns: 14/1; 21/1
C; Superfamily: vitellogenin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Genetics:
A;Gene: BMEII0231
A;Map position: II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
H82699

Hypothestical protein XF1285 [imported] - Xylella fastidiosa (strain 9a5c)

C;Species: Xylella fastidiosa

C;Species: Xylella fastidiosa

C;Pecies: Xylella

R;Andresion: H8269

R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequer

A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: A82515; MuID:20365177

A;Note: for a complete list of authors see reference number A59328 below

A;Return pource: sirtain pastor

A;Return pource: sirtain pastor

A;Residues: 1:56 <SIM>
A;Residues: 1:56 <SIM
A;Residues: Residues: R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Apporthetical protein citG 5'-region - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 16-Dec-1998
C;Accession: B33488
R;Price, V.A.; Feavers, I.M.; Moir, A.
D; Bacteriol. 171, 593-5939, 1989
A;Title: Role of sigma H in expression of the fumarase gene (citG) in vegetative cells A;Reference number: A3488; MUID:90036677
A;Accession: B33488
A;Accession: B33488
A;Accession: B3488
A;Acces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 slyX protein [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 LADAVSKAPQLVPKLDEVYNAAYNAADHAAPEDKYE 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44; DB;
Pred. No. 4.1e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 PKLDEVYNAAYNAADHAAPEDKYEAFVLHFSEALH 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.8%; Score 44; DB Best Local Similarity 22.2%; Pred. No. 4.5e Matches 8; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.8%; Scc
25.7%; Pre
Live 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
-has 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Contents: annotation C; Genetics:
```

11

Q ò

Sed

ð 용

```
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-60 <HEI>
A;Cross-references: GB:AE004391; GB:AE003853; NID:99658015; PIDN:AAF96510.1; GSPDB:GN
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: A53768; S48534
R;Brandt, U.; Uribe, S.; Schaegger, H.; Trumpower, B.L.
J. Blol. Chem. 269, 12947-12953, 1994
A;Title: Isolation and characterization of QCR10, the nuclear gene encoding the 8.5-k
A;Reference number: A53768; MUID:94230378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Introns: 2/3 C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membr F;2-77/Product: ubiquinol--cytochrome-c reductase 8.5K chain *status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: S13450
R; Samakovlis, C.; Kylaten, P.; Kimbrell, D.A.; Engstroem, A.; Hultmark, D.
EMBO J. 10, 163-169, 1991
A;Title: The andropin gene and its product, a male-specific antibacterial peptide in A;Reference number: S13450; MUID:91114699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ubiquinol--cytochrome-c reductase (EC 1.10.2.2) 8.5K chain - yeast (Saccharomyces N;Alternate names: cytochrome bcl complex chain 10; protein YHR001w-a C;Species: Saccharomyces cerevisiae C;Species: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jul-2000
                         A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    andropin precursor - fruit fly (Drosophila melanogaster)
N'Alternate names: antibacterial peptide, male-specific
C.Species: Drosophila melanogaster
C.Species: 19-Mar-1997 #sequence_revision 14-Nov-1997 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Molecule type: DNA
A) Residues: 1-77 <BRA>
A) Cross-references: GB:U07275; NID:g460250; PIDN:AAA19322.1; PID:g460251
C) Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S13450
A; Molecule type: DNA
A; Residues: 1-57 <SAM>
A; Cross-references: EMBL:X56726; NID:g7588; PIDN:CAA40046.1; PID:g7589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 KRNLADAVSKAPQLVPKL--DEVYNAAYNAADHAAPEDKYEAFVLHFSEA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 43; DB 2; Length //;
Pred. No. 7.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26;
                                                                                                                                                                                                                                                                                                                                                                                                                                   10.5%; Score 43; DB 2; 28.0%; Pred. No. 5.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGD:S0003529; MIPS:YHR001w-a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 KAPQLVPKLDEVYNAAYNAADHAAPEDK 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.5%;
Best Local Similarity 39.3%;
Matches 11; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Conservative
Nature 406, 477-483, 2000
A; Title: DNA Sequence of N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references:
A;Map position: 8R
A;Genome: nuclear
                                                                                              A; Accession: E82438
                                                                                                                                                                                                                                                                                                                                         A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: SGD: QCR10
                                                                                                                                                                                                                                                                                C;Genetics:
A;Gene: VCA0609
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                           A;Cross-references: GB:AE004059; GB:AE003849; NID:g9107718; PIDN:AAF85319.1; GSPDB:GN001
A;Experimental source: strain 9a5c
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, E as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, W.C.A.; Ferro, J.A.; Franga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.; Kolliveira, M.C.; de Oliveira, M.V.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, R.N.; Silva Jr., W.A.; da Silvai, A.M.; Silva Jr., W.A.; da Silvai, A;Reference number: A59328
A;Reference number: A59328
A;Contents: annotation
C;Genetics: GGENI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable lipoprotein Cj0818 [imported] - Campylobacter jejuni (strain NCTC 11168)
C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000
C;Accession: B81354
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre
Axittle: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyf
A;Reference number: A81250; MUID:20150912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB73083.1; PID:g696826
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43.5; DB 2; Length 7
Pred. No. 6.6e+02;
8; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 VYNAAYNAADHAAPEDKYEAFVLHFSEALHIIAGTPEVHAVKPG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43.5; DB 2;
Pred. No. 6.5e+02;
4; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 VSKAP-QLVPKLDEVYNAAYNAADHAAPED 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|| | :| ||: | | | : | | | 37 LSKIPEELFPKVLEYINGFYIAHERGLPLD 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.6%;
40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 10.6%;
Best Local Similarity 29.5%;
Matches 13; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.6
Best Local Similarity 40.0
Matches 12; Conservative
                         A; Molecule type: DNA
A; Residues: 1-74 <SI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-75 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics: <GEN2>
A;Gene: XF2521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: XF0687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: Cj0818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

ä

Gaps

10;

cer

ij

Gaps

5;

; ;

> Search completed: July 11, 2002, 10:52:09 Job time: 82 sec

```
SEQUENCE FROM N.A.
                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                            NCBI_TaxID=7227;
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;;
                                                                        01-0CT-1994 (Rel. 30, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Ubiquinol-cytochrome C reductase complex 8.5 kDa protein (EC 1.10.2.2)
(Complex III polypeptide X).
                                                                                                                                                                                                                                                     MEDLINE-94230378; PubMed-8175712;
Brandt U., Uribe S., Schaegger H., Trumpower B.L.;
"Isolation and characterization of QCRIO, the nuclear gene encoding
the 8.5-kDa subunit 10 of the Saccharomyces cerevisiae cytochrome bcl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitochondrion; Inner membrane; Electron transport; Respiratory chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                        ferrocytochrome c.
                                                                                                                                                                                                                                                                                                                                                          SUBUNITS, 2 CORE PROTEINS AND 5 LOW-MOLECULAR WEIGHT PROTEINS -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane. -!- SIMILARITY: TO MAMMALIAN SUBUNIT XI.
                                                                                                                                               Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                         FOR STABLE ASSOCIATION OF THE IRON-SULFUR PROTEIN WITH THE
10 LAIAGSERTQIEPVFSESKTSVYN-----YEAVILN-----GFPE 44
                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: QH(2) + 2 ferricytochrome c = Q + 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.5%; Score 43; DB 1; Length 76; 39.3%; Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E6A01B4F8EF28261 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 AA.
                                                     76 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN-W303 YPH500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 KAPQLVPKLDEVYNAAYNAADHAAPEDK 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KIPLLGPTLE------DHTPPEDK 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                     PRT;
                                                                       01-OCT-1994 (Rel. 30, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oxidoreductase; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U07275; AAA19322.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 AA; 8462 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANDE DROME STANDARD
P21663; Q9VA90;
01-MAY-1991, (Rel. 18, C.
01-MAY-1991, (Rel. 18, L.
16-OCT-2001 (Rel. 40, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S0003529; QCR10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S48534; S48534.
A53768; A53768.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                     NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                   COMPLEX
                                                    UCRX_YEAST
P37299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INIT_MET
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
ANDP_DROME
                                         UCRX_YEAST
рp
                                                              . q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ST T T
```

```
DE MACHOGAIN PRECENTES...

OSCOPOLIA MACHOGAIN PRECENTES...

OSCOSOPALIA MACHOGAINES...

OSCOSOPALIA MACHOGAINES...

ENTRANCAZIA "READAR ACTIONAL ACTIONAL "READARDA" INSECTA:

DEPLYGOTA "MACHOGAINES" ENTRANCAZIA" "READARDA" "READADA" "READARDA" "READARDA" "READARDA" "READARDA" "READARDA" "READADA" "READARDA" "READADA" "READ
```

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

July 11, 2002, 10:51:47; Search time 11.72 Seconds (without alignments) 264.297 Million cell updates/sec Run on:

US-09-696-169A-18 409 1 ADKYKTFEAAFTVSSKRNLA.....SEALHIIAGTPEVHAVKPGA 80 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

8305 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 80

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	crip	P19009 xenopus lae	P37299 saccharomyc			P48274 cyanophora			P09641 myoxocephal	P29206 raja rhina	-	P81028 oreochromis	P44897 haemophilus	Q52278 escherichia	P02821 felis silve	022001 mycobacteri	P26486 azorhizobiu	P57018 bacteriopha	013915 schizosacch	P81455 canis famil	P41459 autographa	_	P09475 lophius ame	P30900 rhodobacter	~	Q38625 bacteriopha		Q9xyz0 conus pulic			Q46789 escherichia	P48860 staphylococ	14	027362 methanobact
SUMMARIES	ID	VTA1_XENLA	UCRX_YEAST	ANDP_DROME	RS20_LACLA	YC34_CYAPA	RL29_SYNP6	YBXH_BACSU	PYY_MYOSC	PYY_RAJRH	OSTC_DRONO	PYY_ORENI	YEJL_HAEIN	KEA1_ECOLI	OSTC_FELCA	VG36_BPMD2	YFXX_AZOCA	Y9K0_BPP22	YDWA_SCHPO	OSTC_CANFA	Y055_NPVAC	MLEV_MOUSE	PPY_LOPAM	ARGD_RHOCA	CERD_CERCA	VG18_BPMU	IPB2_YEAST	CXO1_CONPL	Y059_NPVAC	RECX_THIFE	YGEI_ECOLI	RL7_STAAU	Y058_NPVAC	YD07_METTH
	Length DB	71 1			77 1	7	4	m																								73 1		
de	Query Match Length		10.5	10.4	10.4	10.4		6.6		ø.																						6.0		
	Score	43.5	43	ς.	ς.	42.5	₹	40.5	40	4	39.5	39	39	c	38.5	38	38	38	n	٠	ζ.	37	37	37	37	37	37	37	36.5	36.5	36.5	36.5	36	
	Result No.	1	7	m	4	S	9	7	80	on i	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

δλ

P15936 clostridium P71478 lactobacill Q929x4 rickettsia Q92cr3 rickettsia Q92cr3 rickettsia P20300 pyrococcus P18243 bacteriopha Q9pq2 ureaplasma Q46229 clover prol P80339 thermus aqu Q01784 pisum sativ P33448 saccharomyc P09557 escherichia	S1	1 AA.	7.101-NOV-1990 (Rel. 16, Created) 7.01-NOV-1990 (Rel. 16, Last sequence update) 7.01-NAR-2002 (Rel. 41, Last annotation update) 7.01-NAR-2002 (Rel. 41, Last annotation update) 7.01-NAR-2002 (Rel. 41, Last annotation update) 7.01-NAR-2003 (African clawd frog). 8.01-Naryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; 8.01-Naryota, Mesopatrachia; Pipoidea; Pipidae; 9.01-Naryota, Naryota; Nasobatrachia; Pipoidea; Pipidae; 9.01-Naryota; Naryota; Nasobatrachia; Pipoidea; Pipidae; 9.01-Naryota; Naryota; Na	504704; ten Heggeler B., Brown-Luedi M., de Bony E.,	site	OI FOUR XENORUS 18871S and ONE CALCKEN GENE."; Nucleic Acids Res. 12:8595-8609(1984) -1- FUNCTION: PRECURSOR OF THE MAJOR EGG-YOLK PROTEINS THAT ARE SOURCES OF NUTRIENTS DURING EARLY DEVELOPMENT OF OVIPAROUS	OUGGARDANS. TISSUE SPECIFICITY: PRODUCED BY THE LIVER, SECRETED INTO THE BLOOD AND THEN SEQUESTERED BY RECEPTOR MEDIATED ENDOCYTOSIS INTO GROWING OCCYTES, WHERE IT IS GENERALLY CLEAVED, GIVING RISE TO THE RESPECTIVE YOLK COMPONENTS. INDUCTION: By steroids (estrogen).	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb.ch).		IN A1.	C43881649FF888IA CKC64;  Score 43.5; DB 1; Length 71;  Pred. No. 2.5e+02;  Mismatches 14; Indels 19; Gaps 2;
BCNB_CLOPE CSP1_LACPL RL29_RICCN RL29_RICCN TRM1_PYRW0 Y43_BPR18 RL29_UNEPA RL22_CLOPP RL32_THETH DR39_PEA OM06_YEAST	ALIGNMENT	PRT; 71	ed) sequence upda nnotation up TG Al) (Frag ved frog).  1; Craniata; Mesobatrachi	04704; en Heggeler E	Jenes: compar ceam of the t	one chicken g 3609(1984). THE MAJOR EGG TING EARLY DE	NUCED BY THE RECEPTOR MEIVERALLY CLEAVING.	yyright. It is or of Bloinfor Institute. Institute. It is not remove agreement (§ 1.50 pt.).	5.1; Vitellogenin_N. ogenin_N; 1. phorylation; Signal	VITELLOGENIN A1	C45881049FF8A81A CKC Score 43.5; DB 1; Pred. No. 2.5e+02; 5; Mismatches 14;
8.8 8.8 8.8 8.8 8.8 71 11 8.8 8.8 73 11 8.8 73 11 8.7 73 11 8.8 8.7 73 11 8.7 73 11 8.7 73 11 8.7 73 11 8.7 73 11 8.7 73 11 8.7 73 11 8.7 73 74 74 74 74 74 74 74 74 74 74 74 74 74		STANDARD;	Rel. 16, Create Rel. 16, Last & Rel. 41, Last & All precursor (!) s (African clast tazoa; Chordate tazoa; Chordate racohia; Anura;	TEJUENCE FROM N.A. MEDLINE-85062835; Pubmed-6504704; Germond JE., Walker P., ten Heg	Wahli W.; "Evolution of vitellogenin genes: nucleotide sequences downstream of	us laevis and or Res. 12:8595-8 PRECURSOR OF CREATER DOING	ECIFICITY: PROI SEQUESTERED BY WHERE IT IS GEN E YOLK COMPONEN: By steroids	OT entry is copsistic solutions in the statement this statement this statement incense all to license	EMBL, X01168, CAA25615.1; PIN, X0376, A23876, LiterPro; IPR001347; Vitellogenin_N Pfam; PF01347; Vitellogenin_N; 1. Storage protein; Phosphorylation; S	1 15 16 >71 71 71	1 AA; /82/ MW; 10.6%; larity 29.6%; Conservative
334 335 337 337 338 339 336 336 336 336 336 336 336 336 336		T 1 XENLA VTA1_XENLA	713005) 01-NOV-1990 (101-NOV-1990 (101-NOV-1990 (101-NOV-1990 (101-NOV-1990 (101-NOV-1990)) Amonopus laevii Kenopus laevii Mer Amphibia: Battanyota; Mer Amphibia: Battanyota; Novelopodinae; Novelopodinae; Novelopodinae;	SEQUENCE FROM MEDLINE-850620 Germond JE.	Wahli W.; "Evolution of nucleotide sec	of four Xenopo Nucleic Acids -!- FUNCTION: SOURCES OF	-:- TISSUE SPEC AND THEN SI OOCYTES, WI RESPECTIVE -:- INDUCTION:	This SWISS-PROBLE between the Street the European luse by non-proper modified and entities requires requirements.	EMBL; X01168; PIR; A23876; InterPro; IPR Pfam; PF01347, Storage prote	SIGNAL CHAIN NON_TER	SEQUENCE /1 AA; Query Match Best Local Similarity Matches 16; Conser
		RESULT VTAL_X ID V	S S S S S S S S S S S S S S S S S S S	RP RA RA	RT RT	# # 8 8 8	388888	888888888		FFF	$\alpha \alpha \Sigma$

 $\sim$ 

```
16;
                                                                                                                                                                                                                                                                                                                                                                           Cyanelle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (1997).
                                                                                                                                                       RESULT 5
YC34_CYAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RL29_SYNP6
      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                       qq
                                                                                                                                                                                                    õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lactococcus Tactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AEUCO404; AAAO383.1;
InterPro; IPR002383; Ribosomal_S20p.
Pfam; PF01649; Ribosomal_S20p; 1.
Probom; PD004231; Ribosomal_S20p; 1.
Ribosomal protein; RrM-binding; Complete proteome.
SEQUENCE 77 AA; 8353 MW; 97555044BF145174 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             EEA8CCCF59A09AB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.4%; Score 42.5; DB 1; 36.8%; Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:| | : ||:| || :|||
15 AISVGPSDAVFIDILDKVENAIHNAAQVGIGFAKPFEK 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 AVSKAPQ---LVPKLDEVYNAAYNAAD----HAAPEDK 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
30s ribosomal protein 520.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
                                                                                                                                                                                                                                                                                                                            Signal.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                       ANDROPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21235186; PubMed=11337471;
                                                                                                      EMBL; X16972; CAA34842.1; -
EMBL; X56726; CAA40046.1; -
EMBL; AF018986; AAB82482.1; -
EMBL; AF018989; AAB82486.1; -
EMBL; AF018999; AAB82486.1; -
EMBL; AF018999; AAB82486.1; -
EMBL; AF018992; AAB82489.1; -
EMBL; AF0189373; AAB82489.1; -
EMBL; S13450; S13450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE006404; AAK05837.1; -.
                                                                                                                                                                                                                                                                                                                          Insect immunity; Antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                           57 AA; 6151 MW;
                                                                                                                                                                                                                                                                                                      FlyBase; FBgn0000094; Anp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPST OR LL1739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-IL1403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RS20_LACLA
                                                                                                                                                                                                                                                                                                                                                                       PEPTIDE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O9CEUS;
                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4

RESOLLACLA

ID ACCORDANCE

BY 01-WARD

DT 01
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

Score 42.5; DB 1; Length 77; Pred. No. 3.5e+02;

10.4%; 28.6%;

Query Match Best Local Similarity

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-LB555 / PRINGSHEIM;
Loeffelhardt W., Stirewalt V.L., Michalowski C.B., Annarella M.,
Loeffelhardt W., Stirewalt V.L., Mong S., Newmann-Spallart C.,
Steiner J.M., Jakowitsch J., Bohnert H.J., Bryant D.A.;
"The complete sequence of the cyanelle genome of Cyanophora paradoxa:
the genetic complexity of a primitive plastid.";
(In) Schenk H.E.A., Herrmann R., Jeon K.W., Mueller N.E.,
Schwemmler W. (eds.);
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cyanelle DNA from Cyanophora paradoxa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 YQTIE----ILHKESLSFELDQIVEFEPRKSNIIVNINSSENSIKHEWDVISCESFVLNL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 YKTFEAAFTVSSKRNLADAVSKAPQLVPKLDEV---YNAAYNAADHAAPEDKYEAFVLHF
                                                 13 VSSKRNLADAVSKAPQLVPKL----DEVYNAAYNAADHAAPEDKYEAFVLHFSEA 63
                                                                              Eukaryotism and Symbiosis, pp.40-48, Springer-Verlag, Heidelberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stirewalt V.L., Michalowski C.B., Loeffelhardt W., Bohnert H.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.4%; Score 42.5; DB 1; Length 77; 22.6%; Pred. No. 3.5e+02; ive 15; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Glaucocystophyceae; Cyanophoraceae; Cyanophora
NCBI_TaxID=2762;
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6D4D8686D3B05503 CRC64;
16;
                                                                                                                                                                                                                                                                           01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical 8.9 kDa protein ycf34.
                                                                                                                                                                                                                              Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 36, Created)
(Rel. 36, Last sequence update)
13; Mismatches
                                                                                                                                                                                                                              11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant Mol. Biol. Rep. 13:327-332(1995)
                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U30821; AAA81176.1; -.
Mendel; 7945; CYAPa;ycf34;1.
Cyanelle; Hypothetical protein.
SEQUENCE 77 AA; 8916 MW; 6D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bryant D.A.;
"Nucleotide sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-LB555 / PRINGSHEIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                        Cyanophora paradoxa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RL29_SYNP6
024697;
15-JUL-1998
15-JUL-1998
                                                                                                                                                                                                                           YC34_CYAPA
P48274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l:
SK 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U S E E
```

3

Gaps

7;

Indels

Length 63;

```
MEDLINE-87176585; PubMed-3562898; Conflor J., Schmidt W.E., Gallwitz B., Falkmer S., Thim L.; Confor J.M., Schmidt W.E., Gallwitz B., Falkmer S., Thim L.; Characterization of an amidated form of pancreatic polypeptide from the daddy sculpin (Cottus scorpius).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes; Cottoidei; Cottidae; Myoxocephalus.
                                                                                                                                                                                                             6 TFEAAFTVSSKRNLADAVSKAPQLVPKLDEVYNAAYNAADHAAPEDKYEAFVLHF 60
                                                                                                                                                                                                                                  10 TEQPEFSV-VRQNGAIHVXHQGEFVEEIEFEFNGEY--PDH----DLIEELVNHY 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Pancreas;
MEDLINE=87190954; PubMed=2883025;
Cutfield S.M., Carne A., Cutfield J.F.;
"The amino-acid sequences of sculpin islet somatostatin-28 and peptide YY.";
                                                                                                                                                                                                                                                                                                                                                                            01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
16-COT-2001 (Rel. 40, Last annotation update)
Peptide YY-1ike (PYY).
Myoxocephalus scorpius (Shorthorn sculpin) (Daddy sculpin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fegul. Pept. 16:261-268(1986).
--- SUBCELLULAR LOCATION: Secreted.
--- SIMILARITY: BELONGS TO THE NPY / PPY / PAMILY.
PIR; A603039; YFFIS.
HSSP, P01303; IRON.
InterPro; IPR001955; Pancreatic_hormn.
                                                         Hypothetical protein; Complete proteome.
SEQUENCE 63 AA; 7477 MW; 6160B4700B78146A CRC64;
                                                                                                                                  9.9%; Score 40.5; DB 1;
29.1%; Pred. No. 4.6e+02;
ative 10; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00265; PANCREATIC_HORMONE_1; 1. PROSITE; PS50276; PANCREATIC_HORMONE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00159; hormone3; 1.
PRINTS; PR00278; PANCHORMONE.
ProDom; PD001267; Pancreatic_hormn; 1.
SMART; SM00309; PAH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
   EMBL; X92859; CAA63444.1; -. EMBL; Z99105; CAB12002.1; -. SubtiList; BG11506; ybxH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 AA; 4170 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEBS Lett. 214:57-61(1987).
                                                                                                                                Query Match 9.9%
Best Local Similarity 29.1%
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity >2...
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46 HAAPED--KYEAFVLHF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :|:||| || || |:
11 NASPEDWAKYHAAVRHY 27
                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hormone; Amidation.
                                                                                                                                                                                                                                                                                                                                       PYY_MYOSC
P09641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PYY_RAJRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PYY_RAJRH
                                                                                                                                                                                                                                                                                                                          PYY_MYOSC
                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΩI
     DR
DR
DR
SQ
                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use .by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseélsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-97444291; PubMed-9300823;
Sugita M., Sugishita H., Fujishiro T., Tsuboi M., Sugita C., Endo T.,
                                                                                                                                                                                                         "Organization of a large gene cluster encoding ribosomal proteins in
the cyanobacterium Synechococcus sp. strain PCC 6301: comparison of
gene clusters among cyanobacteria, eubacteria and chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shcheptov M., Chyu G., Bagyan I., Cutting S.M.;
Characterization of csgA, a new member of the forespore-expressed
signad-regulon from Bacillus subtilis.";
Gene 184:133-140(1997).
                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE L29P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                       Synechococcus sp. (strain PCC 6301) (Anacystis nidulans).
Bacteria; Cyanobacteria; Chrococcales; Synechococcus.
NCBL_TaxID=1139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 10.0%; Score 41; DB 1; Length 64; 1 Similarity 32.4%; Pred. No. 4.1e+02; 11; Conservative 5; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-201 (Rel. 40, Last annotation update)
Hypothetical 7.5 kDa protein in CSGA 3'region (ORF3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 AA; 7650 MW; 27D8AE7379FCAB92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
NCBL_TaxID=1423;
16-OCT-2001 (Rel. 40, Last annotation update) 50S ribosomal protein L29. RPMC OR RPL29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 VPKLDEVYNAAYNAADHAAPEDKYEAFVLHFSEA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 LPKIEDVRNLSDADLAEKIAEAKRELFDLRFORA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB000111; BAA22457.1; -.
InterPro; IPR001854; Ribosomal_L29.
Pfam, PF00831; Ribosomal_L29; 1.
PROSTIE; PS00579; RIBOSOMAL_L29; 1.
Ribosomal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97169156; PubMed=9016963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                    Gene 195:73-79(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-168 / PY79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996
01-OCT-1996
16-OCT-2001
                                                                                                                                                                                         Sugiura M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YBXH_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                    genomes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
YBXH_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
1;
                                                                                 Gaps
                                                                                 .;
7
                                                    Score 40; DB 1; Length 36;
Pred. No. 2.8e+02;
Mismatches 3; Indels
AMIDATION.
16F331B73643D7AA CRC64;
```

```
01-NOV-1995
01-NOV-1995
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YEJL_HAEIN
P44897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYY_ORENI
P81028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
PYY_ORENI
ID PYY_OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
YEJL_HAÈIN
                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DI AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Osteocalcin (Gamma-carboxyglutamic acid-containing protein) (Bone Gla-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hug N.L., Tseng A., Chapman G.E.;
"The amino acid sequence of Emu osteocalcin: gas phase sequencing of Gla-containing profess.";
Biochem. Int. 15:271-277(1987).
-!-FUNCTION: CONSTITUTES 1-2% OF THE TOTAL BONE PROTEIN. IT BINDS
STRONGLY TO APATITE AND CALCIUM.
-!- PTW. GAMMA-CARBOXYGLUFAMIC ACID RESIDUES ARE FORMED BY VITAMIN K
DEPENDENT CARBOXYLATION. THESE RESIDUES ARE ESSENTIAL FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                              Raja rhina (Skate).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Blasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
NCBI_TaxID=30478;
                                                                                                                                                                                                                                                                   MEDLINE=91296574; PubMed=2067973;
Conlon J.M., Bjenning C., Moon T.W., Youson J.H., Thim L.;
Conlon J.M., Bjenning C., Moon T.W., Youson J.H., Thim L.;
Neuropeptide Y-related peptides from the pancreas of a teleostean (eel), holostean (bowfin) and elasmobranch (skate) fish.";
Peptides 12:221-226(1991).
-!- SUBCELLIDIAR LOCATION: Secreted.
-!- SIMILARILY: BELONGS TO THE NPY / PPY / PYY FAMILY.
HSSP: P01303; IRON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dromaius novae-hollandiae (Emu).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Palaeognathae; Casuariiformes; Dromaiidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE OSTEOCALCIN / MATRIX GLA-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.8%; Score 40; DB 1; Length 36;
42.9%; Pred. No. 2.8e+02;
ive 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMIDATION.
07A7D9DC196660B6 CRC64;
                        01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Peptide YY-like (PYX).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00265; PANCREATIC_HORMONE_1; 1. PROSITE; PS50276; PANCREATIC_HORMONE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam: PF00159; hormone3; 1.
PRINTS: PR00278; PANCHORMONE.
PRODOM: PD001267; Pancreatic_hormn; 1.
SMART; SM00309; PAH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001955; Pancreatic_hormn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002384; GLA_bone.
InterPro; IPR000294; VitK_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-88134266; PubMed=3501719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 AA; 4251 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 NAADHAAPED -- KYEAFVLHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 42.9 les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BINDING OF CALCIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hormone; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S02208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=8790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein) (BGP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S02208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OSTC_DRONO P15504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
P29206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
OGSTC_DRONO
OGSTC_DRONO
DT 01-APR
DT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
         QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
```

```
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ï
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
Cichlidae; Orecchromis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nguyen T.M., Wright J.R. Jr., Nielsen P.F., Conlon J.M.;
"Characterization of the pancreatic hormones from the Brockmann body
of the tilapla: implications for islet xenograft studies.";
Comp. Biochem. Physiol. 111C:33-44(1995).
-: SUBCELJULAR LOCATION: Secreted.
-: SIMILARITY: BELONGS TO THE NPY / PPY PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
Pfam; PF00594; gla; 1.

RRINTS; PR00002; GLABONE.

RSMART; SM00069; GLA; 1.

RROSITE; PS00011; GLU_CARBOXYLATION; 1.

Ralclum-binding; Gamma-carboxyglutamic acid; Vitamin K; Bone.

And Carboxyglutamic ACID.

GAMMA-CARBOXYGLUTAMIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26
                                                                                                                                                                                                                                                                                                                                                            Score 39.5; DB 1; Length 48;
Pred. No. 4.4e+02;
7; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 AFTVSSKRNLA----DAVSKAPQLVPKLDEVYNAAYNAADHAAPEDKYEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Peptide YY-1ike (PYY).
Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMIDATION (BY SIMILARIT) 0246CFBC6243D7AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB 1; Pred. No. 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS, PRO0278; PANCHORMONE.
Prodom; PD001267; Pancreatic_hormn; 1.
SMART; SM00309; PAH; 1.
PROSITE; PS00265; PANCREATIC_HORMONE_1; 1.
PROSITE; PS50276; PANCREATIC_HORMONE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P01303; IRON.
InterPro; IPR001955; Pancreatic_hormn.
Pfam; PF00159; hormone3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95384941; PubMed=7656183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 32, Created)
(Rel. 32, Last sequ
(Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                         Query Match 9.7%;
Best Local Similarity 27.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 AA; 4201 NW;
                                                                                                                                                                                                                                                                                                                                                                                                             14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 AAPED--KYEAFVLHF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:||| || || || 1:
12 ASPEDWAKYHAAVRHY 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hormone; Amidation.
MOD_RES 36
SEQUENCE 36 AA; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
```

```
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                              78 AA; 8642 MW; 9E82DA15BA6A574E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
17
21
24
29
5495 MW;
                                                                    EMBL; U67194; AAC64427.1; -.
                                                                                                                                 Query Match 9.5%
Best Local Similarity 25.6%
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 34.55
Matches 10; Conservative
                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BINDING OF CALCIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FAMILY.
PIR; A03304; GECT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                                                                      protein) (BGP).
                                                                                                                                                                                                                                                                           OSTC_FELCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOD_RES
MOD_RES
                                                                                Plasmid
                                                                                                                                                                                                                                                                                       P02821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40D_RES
                                                                                                                                                                                                                                                 RESULT 14
OSTC_FELCA
                                                                                                                                                                                                                                                                                                                                                                 BGLAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
       SSSSS¥¥8
                                                                                                                                                                                     ò
                                                                                                                                                                                                           Q
                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
                                                                                                     STRAIN-RD / KW20 / ATCC 51907;
MEDLINE-95350630; PubMed-7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterpost T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli.
Plasmid IncP-beta R751.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89
                                          Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                 "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             11 protein; Complete proteome.
72 AA; 7684 MW; 7220CB06FCC35BC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 NAAYNAADHAAPEDKYEAFVLHFSEALHIIAGTPEVHAVK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NMASNLLTTSVPQTQCEALAQAFSNSL-----INAVK 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39; DB 1; Pred. No. 7.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                          Science 269:496-512(1995).
-!- SIMILARITY: STRONG, TO E.COLI YEJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klea protein (KCRA1 protein)
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U32766; AAC22499.1; -.
Hypothetical protein HI0840.
HI0840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 9.5
Best Local Similarity 30.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                             Haemophilus influenzae
                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                   NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                               TIGR; HI0840;
Hypothetical p
SEQUENCE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLEA OR KCRA1
                                                                                                                                                                                                                                       Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEA1_ECOLI
Q52278;
                                                          Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39
      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
```

```
;;
                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002384; GLA_bone.
InterPro; IPR002294; VitK_dep_GLA.
InterPro; IPR000294; VitK_dep_GLA.
InterPro; IPR00029; GLADNOE.
SMART; SM00069; GLA: 1.
PROSITE; PS00011; GLU_CARBOXYLATION; 1.
PROSITE; PS00011; Gumma-carboxyglutamic acid; Vitamin K; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
0steocalcin (Gamma-carboxyglutamic acid-containing protein) (Bone Gla-
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shimomura H., Kanai Y., Sanada K.;
"Prinary structure of cat osteocalcin.";
J. Biochem. 96:405-411(1984).
-!- FUNCTION: CONSTITUTES 1-2% OF THE TOTAL BONE PROTEIN. IT BINDS
STRONGLY TO APAITTE AND CALCIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- PTM: GAMMA-CARBOXYGLUTAMIC ACID RESIDUES ARE FORMED BY VITAMIN DEPENDENT CARBOXYLATION. THESE RESIDUES ARE ESSENTIAL FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE OSTEOCALCIN / MATRIX GLA-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 49;
Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93D2131FA9F656D3 CRC64;
                                                                                                       2 DKYKTFEAAFTVSSKRNLADAVSKAPQLVPKLDEVYNAAYNAA 44
                                                                                                                                        Score 38.5; DB 1;
Pred. No. 5.8e+02;
3; Mismatches 9;
  9.5%; Score 39; DB 1; ]
25.6%; Pred. No. 8.6e+02;
                                                                                                                                                                                                                                                                                          49 AA
                                                   10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYDROXYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 QLVPKLDEVYNAAYNAADHAAPEDKYEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELNPDCDEL-----ADHIGFQDAYRF
                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=85054706; PubMed=6334077;
```

VG36 BPMD2

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=97419508; PubMed=9274023;
Ribeiro G., Viveiros M., David H.L., Costa J.V.;
Mycobacteriophage D29 contains an integration system similar to that of the temperate mycobacteriophage L5.";
Microbiology 143:2701-2708(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-98300335; PubMed-9636706;
MEDLINE-98300335; PubMed-9636706;
MEDLINE-98300335; PubMed-9636706;
"Caroff N.E., Sarkis G.J., Belanger A.E., Hendrix R.W., Hatfull G.F.;
"Genome structure of mycobacteriophage D29: implications for phage evolution.";
                                                                                                                                                                                                                                                                                                                                                   Mycobacteriophage D29.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI_TaxiD=28369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 9.3%; Score 38; DB 1; Length 56; Best Local Similarity 36.7%; Pred. No. 7.7e+02; Matches 11; Conservative 5; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2214; AAC18477.1; -.
56 AA; 6322 MW; 62C0A18814291847 CRC64;
                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                       56 AA.
                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Mol. Biol. 279:143-164(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U81553; AAB69100.1; -. EMBL; AF022214; AAC18477.1;
                                                       STANDARD;
                                                                                                                                                                                                                                                                                  Gene 36 protein (GP36).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                            36 OR G2
VG36_BPMD2

ID VG36_BS

AC 1022001

DT 15-DEC

DE Gene 3 6 0R

OS Wycoba

OS
```

7 FEAAFTVSSKRNLADAVSKAPQLVPKLDEV 36

ò g Search completed: July 11, 2002, 10:55:16 Job time: 209 sec

```
July 11, 2002, 10:51:27 ; Search time 24.1 Seconds (without alignments) 574.257 Million cell updates/sec
                                                                                                                                                                   US-09-696-169A-18
409
1 ADKYKTFEAAFTVSSKRNLA.....SEALHIIAGTPEVHAVKPGA 80
                                                                                                                                                                                                                                                                                                                                66515
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                        562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPTREMBL_19:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_manmal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_plant:*
sp_rodent:*
sp_virus:*
                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0 Maximum DB seq length: 80
                                                                                                                                                                     Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                                                                                                                                                          Searched:
                                                                                                    Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q91ej4 qlycine max	Q9lej6 glycine max	Q9lej7 glycine max	Q9lej2 glycine max	Q9h360 homo sapien	Q917i8 synechococc	Q98tp3 platichthys	Q16278 homo sapien	Q9pwf9 coturnix co	Q46774 escherichia	Q917h8 synechococc	Q9lxf0 arabidopsis	074989 schizosacch	Q9vys1 drosophila	Q9ccx2 mycobacteri	099013 bacteriopha
SUMMARIES	ID	0 Q9LEJ4	0 Q9LEJ6	0 Q9LEJ7	0 Q9LEJ2	_	2 Q9L7I8		_		046774	_		V	Q9VYS1	16 Q9CCX2	096013
	% Query Match Length DB	2.7 66 1	2.2 66 1	3.2 68 1	2.2 71 1	64	11.9 72 2	79	68	61	64	73	75	77	77	2 79 1	2 80 9
	& Que Score Mat	52 12	50 12	50 12	50 12	49.5 12	48.5 11		48 11	47 11	46 11	46 11	46 11	46 11	46 11	46 11	46 11
	Result No.		7	e	4	5	9	7	89	σ	10	11	12	13	14	15	16

Ogpaig xylella fas Ogpvx9 gallus gall O03907 bacteriopha Ogolly6 leishmania Ogold oryctolagus Ogyaril salvelinus Ogyaril salvelinus Oglej5 glycine max Oglej6 glycine max Oglej6 glycine max Oglej6 glycine max Oglej6 campylobact Oflej6 ceratitis c Oglej6 campylobact Oflej6 ceratitis c Oglej6 secratitis c	STNS	66 AA.	ence update) .ation update) MT).	MSG. Glycine max (Soybean). Elukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine. NCBI_TAXID=3847;	nk/DDBJ databases.	Vodkin L.O.; n a complex developmental pattern base pairs.";	SCDE94F CRC64;	DB 10; Length 66; 1.2e+02; .ches 21; Indels 28; Gaps 4;		LPKGDEHSLVKWTFLYEKVDHTAPEPTKYKDLVV 52
09PAI8 09PVX9 003907 09NLY6 09BDR0 09BDR0 09BBR0 09LEJ5 09LEJ5 09LEJ5 09LEJ5 09LZ6 09LZ6 09LZ6 09LZ7 09BU57	ALIGNMENT	PRT;	(TrEMBLrel. 15, Created) (TrEMBLrel. 15, Last sequence u; (TrEMBLrel. 16, Last annotation PROTEIN HOMOLOGUE (FRAGMENT).	reptophyta ; eudicoty e; Papilic	the EMBL/GenBank/DDBJ	v V O	6E75647455CDE94F	Score 52; Pred. No. 0; Mismatc	YKTFEAAFTVSSKRNLADAVSKAPQLVPKLDE-   ::	LPKGDE
119 119 100 100 100 100 100 100 100 100			15, 15, 16, DLOGU	s; St ohyta oacea	the	ed≖105 raman is ac roxima 7-231(	MM;	.78; .38; e 1	VSKA	
8848777448888868888777889898989771888888947888999999991		PRELIMINARY;	TrembLrel. TrembLrel. TrembLrel.	bean). iplantae ignolior ies; Fal	1. 300) to	Kk, 10; PubMed=10579489 Sundararaman V.P., er that is active it its proximal 650 11:217-231(1999) CAB96763.1;	7727	12 25 tiv	KRNLAD#	
		PRELI	(Tre (Tre (Tre PROTE	(Soyk iridi a; Ma Faba] 847;	ROM N.A. CLARK; .; (JUL-2000)	FROM N.A. V. CLARK; 20044090; 1 M.V., Sunc promoter i without ii 1. Biol. 4 293441; CAl	9	larity Conser	FTVSS	- 1
119		T 1 4 Q9LEJ4 Q9LEJ4;	01-0CT-2000 01-0CT-2000 01-MAR-2001 MAJOR LATEX	MSG. Glycine max Eukaryota, V Spermatophyt. eurosids I;	SEQUENCE FROM N.A. STRAIN=CV. CLARK; Vodkin L.O.; Submitted (JUL-2000)	SEQUENCE FROM N.A. STRAIN=CV. CLARK, MEDLINE=20044090; PubMed=10579489; Stromvik M.V., Sundararaman V.P., "A novel promoter that is active i with and without its proximal 650 Plant Mol. Biol. 41:217-231(1999). MEMBL; AJ293441; CAB96763.1;	SEQUENCE	Query Match Best Local Similarity Matches 20; Conserva	4 YKTFEAA	9 YKSYEVIVHV
HHH00000000000000000000000000000000000		SU		× 0 0 0 0 0 0			ŏs	Oue Bes Mat	Qy	qa

 $^{\circ}$ 

æ,

9 9

```
Spermatophyta; Magnollophyta; eudloctyledons; core eudlocts; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae; Glycine. NCBI_TaxID=3847;
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-CV. WILLIAMS 82; TISSUE-POD;
MEDLINE-20044090; PubMed=10579489;
ASTROMINE M.V., Sundararaman V.P., Vodkin L.O.;
"A novel promoter that is active in a complex developmental pattern with and without its proximal 650 base pairs.";
Plant Mol. Biol. 41:217-231(1999).
EMBL; AJ293445; CAB96766.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang C., Yu Y., Zhang S., Zhou G., Wei H., Bi J., Dong C., Zai Y., Xu W., Gao F., Liu M., He F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                    20 VLPKGDEHSLVKWTFLYEKVDHTAPEPTKYKDLVVKLTKNV-----EAHLVE 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 LVPKLDE----VYNAAYNAADHAAPE-DKYEAFVLHFSEALHIIAGTPEVHAVK 77
                                                                                                                                                                                          29 LVPKLDE----VYNAAYNAADHAAPE-DKYEAFVLHFSEALHIIAGTPEVHAVK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 71;
                                                                                                              Length 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                        D47B0455D46768CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 AA; 8318 MW; DA187778AF5D8925 CRC64;
                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MAJOR LATEX PROTEIN HOMOLOGUE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
                                                                                                                DB 10;
2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 50; DB 10;
Pred. No. 2.1e+02;
9; Mismatches 17
                                                                                                                                                                                                                                                                                                                                    Ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 AA
                                                                                                                Score 50; DB
Pred. No. 2e+0:
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CV. WILLIAMS 82; TISSUE-POD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                    PRT;
Plant Mol. Biol. 41:217-231(1999).
EMBL; AJ293436; CAB96758.1; -.
                                                                                                                  12.2%;
29.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 12.2%;
Best Local Similarity 29.6%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16,
                                                        68 AA; 7940 MW;
                                                                                                                Query Match 12.2
Best Local Similarity 29.6
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycine max (Soybean).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vodkin L.O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
SEQUENCE
                                      NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PR01331.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09н360;
                                                                                                                                                                                                                                                                                                                                  Q9LEJ2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09H360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ß
                                                                                                                                                                                                                                                                                            RESULT
Q9LEJ2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09н360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
  RE
DR
FT
SQ
                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyLedons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine. NCBL_TaxID=3847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stromvik M.V., Sundararaman V.P., Vodkin L.O.;
"A novel promoter that is active in a complex developmental pattern with and without its proximal 650 base pairs.";
Plant Mol. Biol. 41:217-231(1999).
EMBL; AJ293437; CAB96759.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CV. CLARK;
MEDLINE=20044090; PubMed=10579489;
Stromvik M.V., Sundararaman V.P., Vodkin L.O.;
"A novel promoter that is active in a complex developmental pattern with and without its proximal 650 base pairs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 VLPKGDEHSLVKWTFLYEKVDHTAPEPTKYKDLVVKLTKNV-----EAHLVE 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 LVPKLDE----VYNAAYNAADHAAPE-DKYEAFVLHFSEALHIIAGTPEVHAVK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 50; DB 10; Length 66; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 AA; 7726 MW; 607B647455C7494F CRC64;
                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
                                                                                                                                                      66 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Mismatches
                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence
01-MR-2001 (TrEMBLrel. 16, Last annotation
MAJOR LATEX PROTEIN HOMOLOGUE (FRAGMBRY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TIEMBLIE). 16, Last annotati
MAJOR LATEX PROTEIN HOMOLOGUE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequ
(TrEMBLrel. 16, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CV. CLARK;
MEDLINE=20044090; PubMed=10579489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 12.2%;
Best Local Similarity 29.6%;
Matches 16; Conservative
                  59 HFSEALHIIAGTPEVHAVK 77
                                                      53 KLTKNV-----EAHLVE 64
                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Soybean).
                                                                                                                                                                                                                                                                                            Glycine max (Soybean).
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CV. CLARK;
Vodkin L.O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CV. CLARK;
Vodkin L.O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-3847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                          09LEJ6;
                                                                                                                                                      Q9LEJ6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9LEJ7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9LEJ7
```

q

ò

3;

1;

```
Pfam; PF00612; IQ; 1.
SMART; SM00015; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROLACTIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 9; Conser
                                                                                                                                                                                                                                              79 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=93934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ionic channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                myometrium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (FRAGMENT)
                                                                                                                                                                                  NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coturnix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               016278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09PWF9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        016278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O9PWF9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
Q9PWF9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
Q16278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RT RT DR L ST L SO ET S 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
"Functional prediction of the coding sequences of 11 new genes deduced by analysis of cDNA clones from human fetal liver."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Robertson B.R., Tezuka N., Watanabe M.M.;
"Phylogenetic analyses of Synechococcus strains (cyanobacteria) using sequences of 16s rDM and part of the phycocyanin operon reveal multiple evolutionary lines and reflect phycobilin content.";
Int. J. Syst. Evol. Microbiol. 51:861-871(2001).
EMBL: AF223433; ARF60095.1;
InterPro. IPR001659; Phycobilisome.
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Platichthys flesus (European flounder).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii: Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Pleuronectidae; Platichthys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                   64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 72;
                                                                                                                                                                                                             Score 49.5; DB 4; Length 6 Pred. No. 2.2e+02; 8; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 ADAVSKAPQLVPKLDEVYNAAYNAADHAAPEDKYEAFVLHFSEALHII 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 VSSKRNLADAV----SKAPQLVPKLDEVYNAAYNAADHAAPEDKY 53
                                                                                                                                                                                                                                                                                                                                                               Synechococcus sp. PS672.
Bacteria; cyanobacteria; Chroococcales; Synechococcus.
NCBL_TaxID=115754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ACETYL-COA ACETYLTRANSFERASE (EC 2.3.1.9) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        831E5FD7A9CDA95F CRC64;
                                                                                                                          6893 MW; 5435D402BA4D80C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 48.5; DB 2;
Pred. No. 3.3e+02;
5; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=PS672;
MEDLINE=21304427; PubMed=11411708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00502; Phycobilisome; 1
NON_TER 72 72
                                                                                                                                                                                                             12.1%;
28.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=OVARY;
Williams T.D., Chipman J.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7597 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 11.9%;
Best Local Similarity 35.4%;
Matches 17; Conservative
                                                                                                                                                                                                       Query Match 12.1'
Best Local Similarity 28.3'
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                             64 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
SEQUENCE
                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09L718
09L718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q98TP3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
098TP3
AC 098TP3
AC 098TP3
DT 01-JUN-
DT 01-JUN-
DT 01-DEC.
DE ACETYL-
GN ACAT1.
GN ACAT1.
GO EURATYC
OC EURATYC
OC ACATCHOO
OC A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q98TP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
Q9L718
              SORF
                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
"A DNA array to monitor the effects of environmental pollution on European flounder (Platichthys flesus).";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ291983; CAC28941.1; -.
HSSP; P27796; lAFY.
Transferase; Acyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                           Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=95179476; PubMed=7874451;
Boyle M.B., Heslip L.A.;
"Voltage-dependent Na+ channel mRNA expression in pregnant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 68;
                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                      30 VPKLDEVY---NAAYNAADHAAPEDKYEAFVLHFSEALHIIAGTPEVHAV
                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
VOLTAGE-DEPENDENT SODIUM CHANNEL ALPHA SUBUNIT PROTEIN
                                                                                                                                                                                     F49166ED133F2C02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E04A55B4E78BBB5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MXY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                         Score 48.5; DB 13;
Pred. No. 3.6e+02;
5; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 48; DB 4; Le
Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coturnix coturnix japonica (Japanese quail).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recept. Channels 2:249-253(1994)
EMBL; 57592; AAD14203.1; -.
InterPro; IPRO00048; IQ.
Pfam; PP00612; IQ; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.7%;
52.9%;
                                                                                                                                                                                       8192 MW;
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 34.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7878 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 LHIIAGTPEVHAVKPGA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|:| | :|| | || 38 IHMIDGDRDVHATKEGA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
```

ö

ä

```
FBM21_210.
Arabidopsis thallana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
     using
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H.W.
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Bevan M. Murphy G., Ridley P., Hudson S., Bancroft I., Mewes Rudd S., Lencke K., Mayer K.F.X.; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.2%; Score 46; DB 10; Length 75; 26.2%; Pred. No. 6.6e+02; Live 8; Mismatches 23; Indels
                                                                                                                                                                   Length 73;
                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EU Arabidopsis sequencing project;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL353993; CAB89342.1;
Hypothetical protein.
SEQUENCE 75 AA; 7948 MW; CD03354251EC2F99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPCG338.12.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetales; Schizosaccharomycetales.
                                                                                                                           73 AA; 7715 MW; 064987E7B0CB4E9C CRC64;
                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 7.9 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HYPOTHETICAL 8.6 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | | | : | : | : | : | 31 NMKLKVLKPPLIIKPLFFLYNKMPKAGGDVSPVSLISSFMIH 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 NLADAVSKAPQLVPKLDEVYNAAYNAADHAAPEDKYEAFVLH 59
                                                                                                                                                                Query Match 11.2%; Score 46; DB 2; Ler
Best Local Similarity 32.5%; Pred. No. 6.4e+02;
Matches 13; Conservative 5; Mismatches 14;
                                                                                                                                                                                                                                         20 ADAVSKAPQLVPKLDEVYNAAYNAADHAAPEDKYEAFVLH 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                    75 AA.
                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 26.2
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4896
                                                                                                             NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                  09LXF0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         074989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        074989
                                                                                                                                                                                                                                                                                                                    Q9LXF0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13
                                                                                                                                                                                                                                                                                         RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
074989
                                                                                                                                                                                                                                                                                                       09LXF0
    RT RT RT DR DR DR DR DR DR SQ
                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
SEQUENCE FROM N.A.
A Kansaku N., Shimada K.;
Kansaku N., Shimada K.;
Submitted PCR cloning quail prolactin.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
REMBL; AB0310910; BAA03342.1;
RSSP; Q28632; 1AN3.
A HSSP; Q28632; 1AN3.
A InterPro; IPR001400; SOMATOTROPIN.
PFam; PF00103; hormone; 1.
PRNS: PR00103; SOMATOTROPIN.
PRNS: PR00156; SOMATOTROPIN.
NON_TER.
                                                                                                                                                                                                          Length 61;
                                                                                                                                                                                              Score 47; DB 13; Length bired. No. 3.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 46; DB 2; Length 64;
Pred. No. 5.4e+02;
Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Estep P.E., O'Keeffe T., Robison K., Church G.M.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U26536; AAA70098.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synechococcus sp. PS674.
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=115756;
                                                                                                                                                                 6994 MW; 71516EF7E06983EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DBC69B0DF1DAD245 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 AA.
                                                                                                                                                                                                                                                                                                                                                             64 AA.
                                                                                                                                                                                                                                       6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21304427; PubMed-11411708;
Robertson B.R., Tezuka N., Watanabe M.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                69
                                                                                                                                                                                                                                                                                         26
                                                                                                                                                                                                          11.5%;
38.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7275 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
11.2%;
Best Local Similarity 38.9%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19, CPCA (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                               36 PEDKEQAQQIHHEDLLNLVLG
                                                                                                                                                                                                                                                              49 PEDKYEAFVLHFSEALHIIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 PQLVPKLDEVYNAAYNAA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1: | ::::|:| | | 27 PEYTPDVNOLYDALYNKA 44
                                                                                                                                                                                                                                       8; Conservative
                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                   Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-PS674;
                                                                                                                                                                 61 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-K12 EMG2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=562;
                                                                                                                                                     NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9L7H8
Q9L7H8;
                                                                                                                                                                                                                                                                                                                                                       Q46774
Q46774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
                                                                                                                                                                                                                                                                                                                                 RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CPCA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09г/н8
                                                                                                                                                                                                                                                                                                                                             046774
    ò
                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

ö

S

us-09-696-169a-18.closed.rspt

```
EMBL; AE003487; AAF48117.1; -.
Flybase; FBgn0030356; CG18184.
SEQUENCE 77 AA; 8569 MW; EDD29D3203853F54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: July 11, 2002, 10:54:58
 Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Job time: 211 sec
                                                                                                                                                                                                                                                                                                                 Q9CCX2;
                                                                                                                                                                                                                                                                                                09CCX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                Q9CCX2
   RE DR SO
                                                                                                                                                                              δ
                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RA Addams W.D., Celnister S.E., Li P.W., Hoskins R.A., Gocayne J.D.,
RA Addams W.D., Celnister S.E., Li P.W., Hoskins R.A., Galle R.P.,
RA Addams W.D., Celnister S.E., Li P.W., Hoskins R.A., Galle R.P.,
RA George R.A., Lewis S.E., Richards S., Ashburner M. Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeliffer B.D.,
RA Adams W.D., Carl, Rogers Y.-H.C., Blazej R.G., Champe M., Pfeliffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Baytaktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Baytaktaroglu L., Beasley E.M.,
Ballew R.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Burtis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Perraz C., Perriar S., Dunkov B.C., Dunn P.
RA Dodson K., Doup L.B., Downess M., Dugan-Rocha S., Dunkov B.C., Dunn P.
RA Burtis N.C., Barsen B.P., Garria C., Perriar S., Perschman M.P.,
RA Glodek A., Gong F. Gorrell J.H., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Wei M.-H., Ibegwam C.J.,
Jalali M., Kalush F., Karpen G.H., Wei M.-H., Ibegwam C.D.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kratt C., Mortis J., Moshrefi A.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., Dri V., Bacleb J.M.,
Ralmel B.E., Kodira C.D., Kraft C., Mortis J., Mosherson D.,
Ra Melson D.R., Pittman G.S., Pan S., Pollard J., Worles D.K.,
Rabor D.R., Pittman G.S., Pan S., Pollard J., Worles D.K.,
Shue B.C., Siden-Kalmos I., Simpson M., Stupski M.P., Santh T.,
Raliams S.M., Woodage T., Staplecton M., Stupski M.P., Santh T.,
Wang S.Y., Wassarman D.A., Weinstcox R.M., Wann B. S., Shen K., Wann B. S.,
Rander R.K., Shen Kalmos I., Simpson M., Stupski M.P., Santh H.,
Raliams S.M., Woodage T., Worley K.C., Wu D., Yenges B.W., Rubin G.M., Venter E., Wann G., Shen K.,
Rander S.M., Woodage T., Worley K.G., Wu D., Yenges B.W., 
                                                                                                                                                                                            ö
                Lyne M., Wood V., Rajandream M.A., Barrell B.G., Murphy L., Harris D.; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; A1023781; CAA19343.1; -.
Hypothatical protein.
SEQUENCE 77 AA; 8552 MW; B63547696FFNNNAAR CROSS
                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                            Gaps
                                                                                                                                                                                            ;
0
                                                                                                                                                        Score 46; DB 3; Length 77;
Pred. No. 6.8e+02;
                                                                                                                                                                                          12; Indels
                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                               77 AA.
                                                                                                                                                                                        4; Mismatches
                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                         4 YKTFEAAFTVSSKRNLADAVSKAPQL 29
                                                                                                                                                                                                                                                         37 YDTVFKGFSVSLPENAVDALSAHPEI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                      11.2%;
38.5%;
                                                                                                                                                   Query Match
Best Local Similarity 38.54
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   CG18184 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BERKELEY
                                                                                                                                                                                                                                                                                                                                                                 09VYS1;
                                                                                                                                                                                                                                                                                                                                            Q9VYS1
                                                                                                                                                                                                                                                                                                           RESULT 14
Q9VYS1
 ŏ
                                                                                                                                                                                                                                                         g
```

```
2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-TN;
MEDLINB-2112973; PubMed=11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Fellwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Ouail M.A., Rajandream M.A., Rutherford K.M.,
Squares S., Stevens K., Jimon S., Simmonds M., Skelton J., Squares R.,
Barrell B.G.;
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 AFTVSSKRNLADAVSKAPQ-----LVPKLDEVYNAAYN-----AADHAAPEDKYEA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                                                                                                                       24 NFIEQTELSNPCTPAQPEIXSVCHQSSGAQLVSEKYK----FQKALEILSAATEIY 76
                                                                                                                      18 NLADAVSKAPQLVPKLDEVYNAAYNAADHA-APEDKYEAFVLHFSEALHIIAGTPEVH
                                                                       ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 79;
                Length 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Complete proteome.
SEQUENCE 79 AA; 8709 MW; 07611AC1A9A65020 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                Score 46; DB 5;
Pred. No. 6.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.2%; Score 46; DB 16;
24.4%; Pred. No. 7e+02;
Live 14; Mismatches 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
EMBL; AL583918; CAC29800.1; -.
Query Match
Best Local Similarity 20.7%; Pred. No. v.c.
Watches 12; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 FVLHFSEALHIIAGT--PEVHAVKPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----ALHLLASSIDPIPRAKYPG
                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL PROTEIN ML0292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                    (TremBLrel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leproma; ML0292;
                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
```

```
1226, Ap
1226, Ap
9, Appli
9, Appli
                                                                                                                                                             Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                           Sequence 1
                                     Sequence
Sequence
                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/08440861

Patent No. 5710126

GENERAL INFORMATION:
APPLICANT: Kuo, Mei-Chang
APPLICANT: Luqman, Mohammad
TITLE OF INVENTION: ALLERGEN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 20; 0.065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                               US-08-936-165A-361

US-08-900-574-3

US-08-911-64

US-08-178-21

US-08-18-4778-21

US-08-293-284A-10

US-08-140-797-8

US-08-140-797-8

US-08-140-797-8

US-08-140-797-8

US-08-140-861-7

US-08-140-861-7

US-09-968-542C-15

US-09-082-2798-1226

US-09-082-2798-1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 1PC-075 (IMI-040cp)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFHONE: (617) 227-7401
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.9%; Score 65; DB 60.0%; Pred. No. 0.06
                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,861
FILING DATE: 15-MAY-1995
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/106,016
FILING DATE: 31-AUG-193
ATTORNEY/AGGENT INFORMATION:
NAME: AMY E. MANGTAGOLTAS
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 20 amino acids IYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide
internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 15.9
Best Local Similarity 60.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
STATE: Massac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
FRAGMENT TYPE:
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-440-861-12
July 11, 2002, 10:50:47; Search time 12.98 Seconds (without alignments) 150.543 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                         1 ADKYKTFEAAFTVSSKRNLA.....SEALHIIAGTPEVHAVKPGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sednence Sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-440-861-12
US-08-440-861-11
US-08-440-861-13
US-08-440-861-14
US-08-440-861-14
US-08-440-861-10
US-08-440-861-10
US-08-956-307B-17
US-08-956-307B-17
US-08-956-307B-18-18
US-08-174-745A-28
US-08-174-745A-28
US-08-133-885-28
US-08-433-885-28
US-08-410-614-28
US-08-410-614-28
US-08-410-614-28
US-08-410-614-28
US-08-410-614-28
US-08-410-811-15
US-08-410-811-15
US-08-410-811-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5-08-174-745A-20
5-08-195-947-20
5-08-433-885-20
                                                                                                                                                                                                                                                                                                                                                                                                   hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                             231628 segs, 24425594 residues
                                                                                              - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Listing first 45 summaries
                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maximum Match 100%
                                                                                                                                                                                                         US-09-696-169A-18
409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                           seq length: 0 seq length: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                     οŧ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.5
43.5
43
                                                                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                   Total number
                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB 9
Maximum DB 9
                                                                                            OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
9
```

ö

us-09-696-169a-18.closed.rai

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 59; DB 1; Length 20;
Pred. No. 0.37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/08440861
Sequence 13, 101026
Patent No. 13, 101026
GENERAL INFORMATION:
APPLICANT: Griffith, Irwin J.
APPLICANT: Lugman, Mohammad
TITLE OF INVENTION: T CELL EPITOPES OF RYEGRASS POLLEN
TITLE OF INVENTION: ALLERGEN
NUMBER OF SUCUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                      COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,861
FILING DATE: 15-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/106,016
FILING DATE: 31-AUG-1993
ATTORNEY/AGENT INPORMATION:
NAME: Amy E. MANDER 36,207
REFERENCE/DOCKET NUMBER: 19C-075 (IMI-040CP)
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street, suite 510 CITY: Boston Massachusetts
COUNTRY: USA
                         E: LAHIVE & COCKFIELD 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CUCKRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,861
FILING DATE: 15-MAY-1995
FLING APPLICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (617) 227-7400 TELEPAX: (617) 227-5941 INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 ADKFKIFEAAFSESSK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ADKYKTFEAAFTVSSK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide FRAGMENT TYPE: internal
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE &
                                                                                         Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 12; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                    Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02109
                                                                                      STATE: Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                      Sequence 11, Application US/08440861

Sequence 11, Application US/08440861

GENERAL INFORMATION:

APPLICANT: Griffith, Irwin J.

APPLICANT: Griffith, Irwin J.

APPLICANT: Lugman, Mohammad

TITLE OF INVENTION: ALLERGEN

TITLE OF INVENTION: ALLERGEN

CORRESPONDENCE ADDRESS:

ADDRESSE: ADDRESS:

ADDRESSE: ALHIVE & COCKFIELD

STREET: 60 State Street, suite 510

CITY: Boston

STATE: Massachusetts

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: BADACE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: BADACE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: 19 PC-DOS/MS-DOS

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/440,861

FILING DATE: 15-MAY-1995

CLASSIFICATION NUMBER: US/08/440,861

FILING DATE: 11-MAY-1995

CLASSIFICATION NUMBER: US/08/106,016

FILING DATE: 11-MAY-1995

CLASSIFICATION NUMBER: US/08/106,016

FILING DATE: 11-MAY-1995

CHASSIFICATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: 1PC-075 (IMI-040cp)

TELECOMMULICATION INFORMATION:

TELEPHONE: Gill 227-7400

TELEPHONE: Gill 227-7400

TELEPHONE: Gill 227-75941

INFORMATION FOR SED ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 mmino acids

TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08440861
Patent No. 5710126
GENERAL INFORMATION:
APPLICANT: Kuo, Mei-Chang
APPLICANT: Lugman, Mohammad
TITLE OF INVENTION: T CELL EPITOPES OF RYEGRASS POLLEN
NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 62;
                    37 YNAAYNAADHAAPEDKYEAF 56
                                             | |:|||| |: || ||:
| PGLIPKLDTAYDVAYKAAE 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 PQLVPKLDEVYNAAYNAAD 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 15.2
Best Local Similarity 57.9
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-440-861-11
                                                                                                                                                  US-08-440-861-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-440-861-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                    ŏ
                                                           q
```

ö

Gaps

ó

Gaps

ö

```
Sequence 10, Application US/08440861

Patent No. 5710126

GENERAL INFORMATION:
APPLICANT: Grifith, Irwin J.
APPLICANT: Luqman, Mohammad

TITLE OF INVENTION: T CELL EPITOPES OF RYEGRASS POLLEN

TITLE OF INVENTION: A LLERGEN

TITLE OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, suite 510

CITY: Boston

CONTAINMENT OF MASSACHUSELTS
                                                         Length 20;
                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPC-075 (IMI-040cp)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 2.8;
                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                         Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCHWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/440,861
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/106,016
FILING DATE: 31-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAMME: AMNY E. MANDTAGOULES
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/08440861
Patent No. 5710126
GENERAL INFORMATION:
APPLICANT: Griffith, Irwin J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: IP TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 20 aming acids
                                                         13.2%;
60.0%;
                                                                                                                                           57 VLHFSEALHIIAGTPEVHAV 76
                                                                                                                                                                                   1 VTALTEALRVIAGALEVHAV 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.5%;
                                                Query Match
Best Local Similarity 60.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 12.7
Best Local Similarity 62.5
Matches 10; Conșervative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 LATSAAKAPGLIPKLD 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 LADAVSKAPQLVPKLD 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOLECULE TYPE:
FRAGMENT TYPE:
US-08-440-861-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02109
                                                                                                                                                                                                                                                                         US-08-440-861-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
US-08-440-861-9
                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                   qq
                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ολ
                                                                                                                                                                                                                                                                                                                                                                                                                13.7%; Score 56; DB 1; Length 20; ilarity 55.0%; Pred. No. 0.88; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14.
Sequence 14. Application US/08440861
Sequence 14. Application US/08440861
GENERAL INFORMATION:
APPLICANT: Griffith, Irwin J.
APPLICANT: Kuo, Mei-Chang
APPLICANT: Lugman, Mohammad
TITLE OF INVENTION: T CELL EPITOPES OF RYEGRASS POLLEN
TITLE OF INVENTION: ALLERGEN
                                                                    NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 1PC-075 (IMI-040cp)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHÂRACTERISTICS:
LENGTH: 20 amino acids
myber amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Amy E. Mandragouras
REGISTRATION UNBRER: 36,207
REFERENCE/DOCKET NUMBER: IPC-075 (IMI-040cp)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: AGCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,861
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION WAR: US 08/106,016
FILING DATE: 31-AUG-1993
ATTORNEY, AGENT: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street, suite 510
             US 08/106,016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 AAPEDKŸEAFVLHFSEALHI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0
FILING DATE: 31-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-440-861-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
: FRAGMENT TYPE: internal
US-08-440-861-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 11, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
```

Gaps

ö

us-09-696-169a-18.closed.rai

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ij
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: MA
COUNTRY: USA
ZIP: 02110-2804
ZIP: 02110-2804
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,307B
FILING DATE: 22-07T-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
US-08-956-307B-18
Sequence 18, Application US/08956307B
Patent No. 6090911
GENERAL INFORMATION:
APPLICANT: Petka, Wendy A.
APPLICANT: Tirrell, David A.
APPLICANT: Revin P. McGrath
TITLE OF INVENTION: REVERSIBLE HYDROGELS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 RNLADAVSKAPQLVPKL-DEVYNAAYNAADHAAPED 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 49.5; I
Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07880/033001
  US/08/956,307B
                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FASSe, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 0788
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFRAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: FASSe, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 0788
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-8906
                                                                                                                                                                                           TELEFAX: 61// ...
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELERAX: 617/24. ..
TELEX: 20154
INFORMATION FOR SEQ ID NO: 18
SEQUENCE CHARACTERISTICS:
STOUGH 76 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                  12.1%;
33.3%;
APPLICATION NUMBER: US/0 FILING DATE: 22-0CT-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 12.19
Best Local Similarity 33.39
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: peptide US-08-956-307B-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 50; DB 1; Length 20;
Pred. No. 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                    TITLE OF INVENTION: T CELL EPITOPES OF RYEGRASS POLLEN VITLE OF INVENTION: ALLERGEN NUMBER OF SEQUENCES: 56 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                         COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCIT Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,861
FILING DATE: 15-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/106,016
FILING DATE: 31-A0G-1993
ATTORNEY/AGENT INFORMATION:
NAME: AMMY E. MANGTAGOULTAS
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
TELLECOMMUNICATION INFORMATION:
TELLECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEXIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFRWARE: FastSEQ for Windows 95
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/08956307B
Patent No. 6090911
GENERAL INFORMATION:
APPLICANT: Petka, Wendy A.
APPLICANT: Tirrell, David A.
TITLE OF INVENTION: REVERSIBLE HYDROGELS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                 E: LAHIVE & COCKFIELD 60 State Street, suite 510
Kuo, Mei-Chang
Lugman, Mohammad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 12.2%;
Best Local Similarity 60.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 FEAAFTVSSKRNLADAVSKA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-440-861-9
                                                                                                                                   STREET: 60 State Stre
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
OGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RY: USA
02110-2804
                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΜA
                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-956-307B-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: M
COUNTRY:
                                                                                                                                                                                             COUNTRY:
```

δ q

ä

g

```
Sequence 28, Application US/08174745A
Patent No. 5736362
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hough, Terryn
Suphioglu, Cenk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 13 amino acids
amino acid
3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 11.7
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: peptide US-08-174-745A-28
                                                                                                                                                                                                                                                                                                               STREET: One Libert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 IAGALEVHAVKP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 IAGTPEVHAVKP 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
US-08-195-947-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                             APPLICANT: Singh, Mohan Bir
APPLICANT: Singh, Mohan Bir
APPLICANT: Singh, Mohan Bir
APPLICANT: Smith, Penelope
APPLICANT: Aviloglu, Asil
APPLICANT: Thecrakulpisut, Piyada
APPLICANT: Suphioglu, Cerry
APPLICANT: Suphioglu, Cerk
APPLICANT: Suphioglu, Cerk
APPLICANT: Suphioglu, Cerk
APPLICANT: Negrass Pollen Allergen
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5721119ris
STRRET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                          ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                11.9%; Score 48.5; DB 3; Length 76; 33.3%; Pred. No. 45;
                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.7%; Score 48; DB 1; Length 13; 83.3%; Pred. No. 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: PA
COUNTRY: USA
ZIP: 19103
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/433,854
FILING DATE:
                                                                                                        7; Mismatches
                                                                                                                                              17 RNLADAVSKAPQLVPKL-DEVYNAAYNAADHAAPED 51
                                                                                                                                                                         |:| | :: | |:| :| | 35 RSLKDKAAELKQEVSRLKNEIEDLKAKIGDHVAPRD 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNBER: US 07/930,060
FILLING DATE: 14-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: HOhenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: IMPH-0024
TELECOMMUNICATION INFORMATION:
TELEPRAX: (215) 568-3409
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                        Sequence 28, Application US/08433854 Patent No. 5721119
                                                                                                        12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 IAGTPEVHAVKP 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IAGALEVHAVKP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
US-08-956-397B-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
US-08-174-745A-28
                                                                                                                                                                                                                                                RESULT 10
US-08-433-854-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-433-854-28
                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
```

```
Gaps
                                                                                                                                                     APPLICANT: Hough, Terryn
APPLICANT: Suphioglu, Cenk
APPLICANT: Ong, Eng Kok
TITLE OF INVENTION: Ryegrass Pollen Allergen
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5736362ris
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Rolease #1.0, Version #1.25
CURRENT APPLICATION DAYN:
APPLICATION NUMBER: US/08/174,745A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ong, Eng Kok
TITLE OF INVENTION: Ryegrass Pollen Allergen
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: IMPH-0024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 28, Application US/08195947; Patent No. 5840316; GENERAL INFORMATION: APPLICANT: Singh, Mohan Bir APPLICANT: Knox, Robert B. APPLICANT: Applicant: Penelope; APPLICANT: Aylioglu, Asil APPLICANT: Theerakulpisut, Piyada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,060
FILING DATE: 14-AUG-1992
ATTORNEY/AGENT INFORMATION:
GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir
APPLICANT: Knox, Robert B.
APPLICANT: Smith, Penelope
APPLICANT: Avjioglu, Asil
APPLICANT: Theerakulpisut, Piyada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
```

ö

ŏ

```
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                          Query Match 11.7
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-433-885-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 IAGTPEVHAVKP 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IAGALEVHAVKP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-08-433-908B-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-433-908B-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5840316ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 13
                                                                                                                             COMPUTER READABLE FOWM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,947
FILING DATE: 14-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,060
FILING DATE: 14-A0G-1992
ATTORNEY ACENT INFORMATION:
NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: MPH-0024
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFHONE: (215) 568-3100
TELEFHONE: (215) 568-3100
TELEFRATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,885
FILING DATE: 02-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 28, Application US/08433885
Fatent No. 586933
GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir
APPLICANT: Singh, Mohan Bir
APPLICANT: Smith, Penelope
APPLICANT: Avjioglu, Asil
APPLICANT: Theerakulpisut, Piyada
APPLICANT: Hough, Terryn
APPLICANT: Suphioglu, Cerk
APPLICANT: Suphioglu, Cerk
APPLICANT: Suphioglu, Cerk
APPLICANT: Suphioglu, Cerk
APPLICANT: Ong, Eng Kok
ITILE OF INVENTION: Ryegrass Pollen Allergen
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSE: Lahive & Cockfield
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 48; DB 2;
Pred. No. 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 11.7%;
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-195-947-28
                                                                                                      ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 IAGTPEVHAVKP 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 60 St
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TIRE: FIDEPY ULSA.
COMPUTER: IEM PC COMPAILDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/43,908B
FILING DATE: 02-MAY-1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: MANDER 36,207
REGISTRATION NUMBER: 36,207
REGISTRATION NUMBER: 1MI-039C2D4
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 742-4214
INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 28, Application US/08433908B
Patent No. 5965455
GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir
APPLICANT: Singh, Penelope
APPLICANT: Smith, Penelope
APPLICANT: Theerakulpisut, Payada
APPLICANT: Theerakulpisut, Payada
APPLICANT: Theerakulpisut, Payada
APPLICANT: Theerakulpisut, Cenk
APPLICANT: Ong, Eng Kok
TITLE OF INVENTION: Ryegrass Pollen Allergen
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield, LLP
STATE: MA
COUNTRY: USA
ZIP: MA
                                                                                                                                                                                                                                                                                                                                                                                                             Score 48; DB 2;
Pred. No. 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/POCKET NUMBER: 1MI-039C2D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
```

ö

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Woodcock Washburn Kurtz Macklewicz & No. 6277383ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA.
                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
              11.7%; Score 48; DB 2; Length 13; 83.3%; Pred. No. 5; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
11.7%; Score 48; DB 4; Length 13;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,614
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/195,947
FILING DATE:
APPLICATION NUMBER: US 07/930,060
FILING DATE: 14-REB-1994
APPLICATION NUMBER: US 07/930,060
FILING DATE: 14-ANG-1992
ATTORNEY/AGENT INFORMATION:
NAME: HORDASCHULZ, LIZA D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: IMPH-0024
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRATICN NUMBER: 33,712
REFERENCE/DOCKET NUMBER: IMPH-0024
TELECOMMUNICATION INFORMATION:
TELEPRATICN NUMBER: 1000
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                        Sequence 28, Application US/08410614

Patent No. 6277383

GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir
APPLICANT: Knox, Robert B.
APPLICANT: Smith, Penelope
APPLICANT: Theerakulpisut, Piyada
APPLICANT: Theerakulpisut, Piyada
APPLICANT: Hough, Terryn
APPLICANT: Gng, Eng Kok
TITLE OF INVENTION: Ryegrass Pollen Allergen
NUMBER OF SEQUENCES: 53
ANDRESEPPERSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 13 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-410-614-28
Query Mat;h
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                   67 IAGTPEVHAVKP 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 IAGTPEVHAVKP 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IAGALEVHAVKP 12
                                                                                                                                                                                                                      RESULT 15
US-08-410-614-28
                                                                                                        οý
                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dp
```

Search completed: July 11, 2002, 10:51:45 Job time: 58 sec

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

July 11, 2002, 10:54:27; Search time 18.25 Seconds (without alignments) 300.115 Million cell updates/sec Run on:

US-09-696-169A-19

Perfect score: Sequence:

SKAPQLVPKLDEVYNAAYNA.....SEALHIIAGTPEVHAVKPGA

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

14670 Total number of hits satisfying chosen parameters:

283138 seqs, 96089334 residues

Searched:

seq length: 0 seq length: 57 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
1: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	a1		leukotriene-A4 hyd	hypothetical prote	0	hypothetical prote	O	hypothetical prote	,	single stranded DN	hypothetical prote	al	,	hypothetical prote	=	hypothetical prote			hypothetical prote	protein disulfide-	hypothetical prote	hypothetical prote	0	hypothetical prote	conserved hypothet	hypothetical prote		-
SUMMARIES	ID	F82545	н82699	YYFIS	S70651	S52358	R3KM72	E84079	S13450	A82732	GECT	S50084	G95302	B41397	A26781	T36238	138225	A90882	G64893	H85736	AG2267	A33210	D83811	AC2208	A61078	E71901	A69871	D69141	508	A95019
	DB	7	~	Н	~	7	~	7	7	~	Н	7	7	7	7	7	7	7	7	7	~	7	7	7	~	7	7	7	7	7
	Query Match Length	54	26	36	49	43	52	99	57	57	49	41	53		37	42	46	55	52	22	52	27	39	52	46	48	45	36	39	42
, de	Query Match	15.3			13.5	•	13.1	13.1	13.1		13.0	•	•	12.5	•	•	•		Ŕ	12.5	ď.		ς.			12.1				11.8
	Score	45.5	44	40	40	39	39	39	39	m	38.5	38	38	37	37	37	37	37	37	37	m	36.5	36.5	36.5	36	36	35.5	32	35	35
	Result No.	1	7	æ	4	S	9	7	œ	6	10	11	13	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

melA protein - Sal	hypothetical prote	hypothetical prote	cholecystokinin/ga	osteocalcin - emu	osteocalcin - crab	osteocalcin - rabb	hypothetical prote	uncharacterized pr	hypothetical prote	MHC HLA-DR-beta-1	ribosomal protein	nitrate reductase	insulin - sperm wh	insulin - finback	ínsulin – seí whal
S42852	A83629	T05086	S24142	802208	GEMKI	A61280	B87570	E97235	A82359	137543	R5VF32	A47694	INWHP	INWHE	INWHIS
7	~	~	7	7	-	Н	7	7	~	7	٦	7	ı	П	1
43	46	46	47	48	49	49	53	52	39	42	48	20	51	51	51
11.8	11.8	11.8	11.6	11.6	11.6	11.6	11.6	11.6	11.4	11.4	11.4	11.4	11.4	11.4	11.4
35	35	35	34.5	34.5	34.5	34.5	34.5	34.5	34	34	34	34	34	34	34
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

```
A; Cross_references: GB:AE004060; GB:AE003849; NID:g9107735; PIDN:AAF85327.1; GSPDB:GN
A; Cross_references: strain 9a5c
B; Experimental source: strain 9a5c
B; Simpson, A.JG: Reinard, F.C.; Arruda, P.; Abreu, F.A.; Acenclo, M.; Alvarenga, R.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Franca, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
chado, M.A.; Madeira, A.M.B.N.; Matchins, E.M.F.; Marino, C.L.; Marques, M.V.; Martins
A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
A; Authors: da Silva, A.C.R.; da Silva, R.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, M.S.; Teuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
A; Reference number: A59328
                                                                                                                                                                                                                   Rianonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq Nature 406, 151-157, 2000
Affilie: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: F82545
hypothetical protein XF2529 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C;Accession: F82545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-54 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Contents: annotation C; Genetics:
```

Gaps ;; Length 54; 22; Indels DB 2; 15.3%; Score 45.5; D 30.2%; Pred. No. 93; ive 7; Mismatches Query Match Pest Local Similarity 30.2% 11: Conservative

ij

### 26 15 NAAYNAADHAAPE-DKYEAFVLHFSEALHIIAGTPEVHAVKPG ò

## g

RESULT 2
H82699
H82699
H82699
H82699
C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000
C;Accession: H82699
E;Accession: H82699
E;Accession: H82699
H;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq Nature 406, 151-157, 2000

us-09-696-169a-19.closed.rpr

```
ribosomal protein S7-2 - Chlamydomonas reinhardtii chloroplast
C;Species: chloroplast Chlamydomonas reinhardtii
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 22-Jun-1999
C;Accession: S11897
R;Robertson, D.; Boynton, J.E.; Gillham, N.W.
Mol. Genc. Genett, 221, 155-163, 1990
A;Tille: Cotranscription of the wild-type chloroplast atpE gene encoding the CF(1)/CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
C;Accession: S52358
R;Agryrokastritis, A.; Leversha, M.A.; Ferguson-Smith, M.; Moschonas, M.K.
submitted to the EMBL Data Library, March 1993
A;Bescription: A cosmid clone mapped to human chromosome 11p15 detects a Taq I restri
                                                                                                                                                                                                    C; Species: Homo sapiens (man)
C; Species: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 07-May-1999
C; Accession: 370651
R; Jendraschak, E.; Kaminski, W.E.; Kiefl, R.; von Schacky, C.
Biochem J. 314, 733-737, 1996
A; Title: The human leukotriene A; Reference number: S70627; MUID:96177841
A; Accession: S70621
A; Molecule type: DNA; MRNA
A; Residues: 1-49 <JEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-43 <AGR>
A;Cross-references: EMBL:X72882; NID:9667005; PIDN:CAA51394.1; PID:9667006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-52 <ROB>
A; Residues: 1-52 <ROB>
C; Cross-references: EMBL:X53977; NID:g11429; PIDN:CAA37927.1; PID:g11430
C; Genetics:
A; Genome: chloroplast
C; Superfamily: Chlamydomonas chloroplast ribosomal protein S7-2
                                                                                                                                                                 leukotriene-A4 hydrolase (EC 3.3.2.6) short isoform - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 4.6e+02;
4; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:U43411
C;Superfamily: leukotriene-A4 hydrolase
C;Keywords: alternative splicing; ether hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB 1; Pred. No. 4e+019; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 13.1%; Score 39; Best Local Similarity 36.7%; Pred. No. 4 Matches 11; Conservative 4; Mismatcl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 VPKLDEVYNAAYNAADHAAPEDKYEAFVLH 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 AAPEDKYEAFVLHFSEALHIIAGTPEVHAV 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: S11897; MUID:90318312
A; Accession: S11897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.5%;
33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 33.38
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-43 <AGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: S52358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                 A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1:56 < SINA
A; Coss-references: GB: AE003962; GB: AE003849; NID: G9106270; PIDN: AAF84094.1; GSPDB: GN001
A; Experimental source: strain 9a5c
R; Simpson, A.J. G.; Reanach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Asubmitted to GenBank, June 2000
A; Authors: Erreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr Chado, M.A.; Martins, E.M.F.; Martino, C.L.; Marques, M.V.; Martins, F.G.; Nunes, L.R.; Oliveira, M.A.; Ge Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Atthores: Martins, E.M.F.; All Sea, A.J.; de N.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Santelli, R.V.; Santalli, R.V.; Santelli, R.V.; Santalli, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.Experimental source: islet organs (Brockmann bodies)
C:Comment: Peptide YY and pancreatic peptide are identical in this fish but are distinct
C:Comment: The protein has been demonstrated in the pyloric but not the splenic Brockman
C:Superfamily: pancreatic hormone
C:Keywords: amidated carboxyl end; hormone; pancreas
F:36/Modified site: amidated carboxyl end (Tyr) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N.Alternate names: pancreatic hormone; pancreatic polypeptide
C;Species: Myoxocephalus scorpius (shorthorn sculpin, daddy sculpin)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 20;Mar-1998
C;Accession: A60309; B26993
R;Conlon, J.M.; Schmidt, W.E.; Gallwitz, B.; Falkmer, S.; Thim, L.
Rsegul. Pept. 16, 261-268, 1986
A;Title: Characterization of an amidated form of pancreatic polypeptide from the daddy A;Reference number: A60309; MUID:87176585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 1-36 <CON>
A; Experimental source: islet organs (Brockmann bodies)
B; Cutifield, S.M.; Carne, A.; Cutifield, J.F.
FEBS Lett. 214, 57-61, 1987
A; Title: The amino-acid sequences of sculpin islet somatostatin-28 and peptide YY.
A; Reference number: A91376; MUID:87190954
A; Recession: B26993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
A,Title: The genome sequence of the plant pathogen Xylella fastidiosa. A,Reference number: A82515; MUID:20365717 A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 1; Length 36;
Pred. No. 2.8e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.8%; Score 44; DB 2; I
25.7%; Pred. No. 1.5e+02;
Live 10; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 PKLDEVYNAAYNAADHAAPEDKYEAFVLHFSEALH 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide YY - shorthorn sculpin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :|:||| || || |:
11 NASPEDWAKYHAAVRHY 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAAPED -- KYEAFVLHF 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein A; Residues: 1-36 <CUT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Contents: annotation C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A60309
                                                                                                                      A; Accession: H82699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: XF1285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQ
```

1;

Gaps

5

Length 43;

5

Gaps

4

Indels

Length 49;

යු

```
A;Cross-references: GB:AE003940; GB:AE003849; NID:g9105966; PIDN:AAF83840.1; GSPDB:GN A;Experimental source: strain 956
R;Simpson, A.J.G.; Reinach, E.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La chado, M.A.; Madelara, A.M.B.N.; Madelara, A.M.B.N.; Madelara, A.Y.; Manthors: M.V.; Marthors: Matthors: Matthors: Matthors: M.Y.; Matthors, M.Y.; Matthors, M.Y.; Matthors, C.E.; Miyaki, C. F.G.; Nunes, L.R.; Oliveira, A.Y.; Menok, C.F.M.; Miracca, E.C.; Miyaki, C. F.G.; Nunes, L.R.; Oliveira, A.Y.; Menok, C.F.M.; Miracca, E.C.; Miyaki, C. F.G.; Santelhors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.M.; Silva Jr., W.B.; Sava A.M.Contents: annotation
                                                                                                                                                                                                                                                                                                                    Rianonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717
A:Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N; Alternate names: BGP; bone Gla protein; gamma-carboxyglutamic acid-containing prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F:97Modified site: 4-hydroxyproline (Pro) #status experimental
F:17,21,24/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental
F:23-29/Disulfide bonds: #status experimental
                                                                                                                                                                 hypothetical protein XF1030 [imported] - Xylella fastidiosa (strain 5doc) C; Species: Xylella fastidiosa C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Felis silvestris catus (domestic cat)
C;Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 06-Sep-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Keywords: bone; calcium binding; carboxyglutamic acid; hydroxyproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.1%; Score 39; DB 2; Length 57; 34.8%; Pred. No. 6.3e+02; rive 6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.0%; Score 38.5; DB 1; 34.5%; Pred. No. 6.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Shimomura, H.; Kanai, Y.; Sanada, K.
J. Biochem. 96, 405-411, 1984
A;Pitle: Primary Structure of cat osteocalcin.
A;Reference number: A03304; MUID:85054706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 QLVPKLDEVYNAAYNAADHAAPEDKYEAF 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | | | ::::|:| : | | | 36 KRECFEINYFDAMHQV--EPSVH 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 KYEAFVLHFSEALHIIAGTPEVH 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: osteocalcin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A03304
A; Molecule type: protein
A; Residues: 1-49 <SHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Accession: A82732
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-57 <SIM>
                                                                                                                                                                                                                                                                                     C; Accession: A82732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: A03304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   osteocalcin - cat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: XF1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       andropin precursor - fruit fly (Drosophila melanogaster)

N.Alternate names: antibacterial peptide, male-specific
C; Species: Drosophila melanogaster
C; Date: 19-War-1997 #sequence_revision 14-Nov-1997 #text_change 21-Jul-2000
C; Accession: S13450
EMBO J. 10, 163-169, 1991
A; Title: The andropin gene and its product, a male-specific antibacterial peptide in Drc
A; Reference number: S13450, MUID: 91114699
A; Reference number: S13450
A; Molecule type: DNA
A; Residues: 1.57 csAM>
A; Residues: 1.57 csAM>
A; Cross-references: EMBL:X56726; NID: 97588; PIDN: CAA40046.1; PID: 97589
A; Note: the authors translated the codon ATT for residue 44 as Thr
C; Comment: This protein is male-specific.
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Cross-references: EMBL:X56726; NID: 97589
A; Introns: 32/3
C; Keywords: antibacterial
F; 1-23/Domain: signal sequence #status predicted <AIC>
F; 24-57/Product: andropin #status predicted <AMT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
E84079
hypothetical protein BH3437 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: E84079
R;Takami, H;Nakasone, K;Takaki, Y;Maeno, G;Sasaki, R;Masui, N;Fuji,F;Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650;MUID:20512582;PMID:11058132
A;Accession: E84079
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-56 <STO>
A;Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BAB07156.1; GSPDB:GNOC
C;Genetics:
A;Gene: BH3437
                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
                                                                                                                                                                                                                                                                                                                               6 LVPKLDEVYNAAYNAADHAAPEDKYEAFVLHFSEALHIIAGTPEVHAVKP 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.1%; Score 39; DB 2; Length 57; 45.8%; Pred. No. 6.3e+02; ive 3; Mismatches 6; Indels
                                                                                                                                  13.1%; Score 39; DB 1; Length 52; 30.0%; Pred. No. 5.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.1%; Score 39; DB 2; Length 56; 37.5%; Pred. No. 6.1e+02; tive 2; Mismatches 13; Indels
                                                                                                                                                                                                               Indels
C; Keywords: chloroplast; protein biosynthesis; ribosome
                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 LDEVYNGGRRPAYHPKMMTKIQLY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 LDEVYNAAYNAADHAAPEDKYEAF 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 9; Conserva
                                                                                                                                                                     Local Similarity
                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53
```

δ q ή;

1;

```
C; Accession: T36238
R; Ollyer, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A submitted to the EMBL Data Library, March 1999
A; Reference number: 221577
A; Accession: T36238
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-42 < OLL>
A; CLSS-references: EMBL:AL049573; PIDN:CAB40336.1; GSPDB:GN00070; SCOEDB:SCE39.28
                                                                                                                 murine transforming growth factor-beta3 (TG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and neuropeptide YY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide YG - American goosefish
C;Species: Lophius americanus (American goosefish)
C;Decies: Lophius americanus (American goosefish)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 12-Apr-1995
C;Accession: A26781
R;Andrews, P.C.; Hawke, D.; Shively, J.E.; Dixon, J.E.
Endocrinology 116, 25677-2681, 1985
A;Title: A nonamidated peptide homologous to porcine peptide YY and neuropep
A;Reference number: A26781; MUID:85203740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-Dec-1999
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 03-May-1994
C;Accession: B41397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                       Riwiller, D.A.; Lee, A.; Matsui, Y.; Chen, E.Y.; Moses, H.L.; Derynck, R. Mol. Endocrinol. 3, 1926-1934, 1989
A; Title: Complementary DNA cloning of the murine transforming growth factot tissues.
A; Reference number: A41397; MUID:90190650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein SCE39.28 - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                    Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 37; DB 2; Level Pred. No. 6.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 2; Le
Pred. No. 6.2e+02;
4; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.5%; Score 37; DB 2; Le
ilarity 58.3%; Pred. No. 7.8e+02;
Conservative 1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: strain A3(2)
C; Genetics:
A; Gene: SCOEDB: SCE39.28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A26781
A; Molocule type: protein
A; Residues: 1-37 <AND>
C; Superfamily: pancreatic hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.5%;
                                                                                                                                                                                                                                                                                                                                                                                                 12.5%;
llarity 37.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 47.1%
2. 8. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 HAAPED -- KYEAFVLHF 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|:||| |:||:
11 NASPEDWASYQAAVRHY 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :| : | : |:|| |
16 YFVQGLPALPGSPEAH 31
                                                                                                                                                                                                                                                                                                                      A; Cross-references: GB: M32745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 HFSEALHIIAGTPEVH 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 GTPEVHAVKPGA 57
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                  A, Accession: B41397
A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-34 <MIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein SMa0625 [imported] - Sinorhizobium meliloti (strain 1021) magaplasm C; Species: Sinorhizobium meliloti
C; Species: Stanorhizobium meliloti
C; Species: Stanorhizobium meliloti
C; Species: Stanorhizobium meliloti
C; Species: Sinorhizobium meliloti
C; Species: Sinorhizobium meliloti
R; Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
S; Kalman, S.; Kaating, D.H.; Pellm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A; Reference number: A95262; MUID:21396509; PMID:11481432
A; Reference number: A95262; MUID:21396509; PMID:11481432
A; Status: preliminary
A; Molecule type: DNA
A; Restause: Dreliminary
A; Molecule type: DNA
A; Restause: GB: AED06469; PIDN:AAK64985.1; PID:914523412; GSPDB:GN00165
A; Status: preliminary
A; Cowse: references: GB: AED06469; PIDN:AAK64985.1; PID:914523412; GSPDB:GN00165
A; Cross-references: GB: AED06469; PIDN:AAK64985.1; PID:914523412; GSPDB:GN00165
A; Cross-references: GB: AED06469; PIDN:AAK64985.1; PID:914523412; GSPDB:GN00165
A; Cowser, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Pela, D; Chanin, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Rederspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.A., A; Reference number: A66039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                   Se
                                                                                                                                                                                                                                                                                                                                                ជ
                                                                                                                                     single stranded DNA-binding protein H16 - green monkey (fragments)
N;Alternate names: RNA-binding protein K homolog
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 23-May-1997 #sequence_revision 23-May-1997 #text_change 19-Feb-1999
C;Accession: S50084
R;Gaillard, C.; Cabannes, E.; Strauss, F.
Nucleic Acids Res. 22, 4183-4186, 1994
A;Title: Identity of the RNA-binding protein K of hnRNP particles with protein H16, a A;Reference number: S50084; MUD:95023188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38; DB 2; Length 53;
Pred. No. 7.7e+02;
2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38; DB 2; Length 41;
Pred. No. 5.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.8%; Scor.
41.2%; Pred No. 5...
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
  ----ADHIGFQDAYRRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B41397
hypothetical protein 1 - mouse
C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S50084
A; Molecule type: protein
A; Residues: 1-16:17-28;29-41 cGAI>
A; Experimental source: cell line CVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.8%;
41.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 YNAAYNAADHAAPEDKY 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 YNASVXVPDXXGPEGSY 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 AFVLHFSEALHIIAGTP 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||:| :| :| || |
18 AFMLFLQSVVHAFAGQP 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Contents: annotation C; Genetics:
24 ELNPDCDEL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: SMa0625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1/3
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
```

qq

8 GVPSRHAVREGA 19

Search completed: July 11, 2002, 10:56:37 Job time: 130 sec

```
A Conlon J.M., Schmidt W.E., Gallwitz B., Falkmer S., Thim L.;
Conlon J.M., Schmidt W.E., Gallwitz B., Falkmer S., Thim L.;
T. "Characterization of an amidated form of pancreatic polypeptide from the daddy sculpin (Cottus scorpius).";
T. Regul. Pept. 16:261-268(1986).
C. -! - SUBCELLULAR LOCATION: Secreted.
-! - SIMILARITY: BELONGS TO THE NPY / PPY / PTY FAMILY.
R PIR; A60309; YYFIS.
R HSSP; P01303; 1RON.
R InterPro; 1PR001955; Pancreatic_hormn.
R PFAMILY: PR001955; Pancreatic_hormn.
R PRINTS; PR00278; PANCHORMONE.
R PRODOM; PD001267; Pancreatic_hormn; 1.
R PROSTITE; PS00265; PANCREATIC_HORMONE_1; 1.
R PROSTITE; PS00265; PANCREATIC_HORMONE_2; 1.
                                          devario pat
puntius tet
                                                                                drosophila
axinella po
                                                                                                           lepisosteus
                                                                                                                     rana ridibu
                                                                                                                                      canis famil
                                                                                                                                               bacteriopha
                               danio kerri
                                                                     bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                        PYY_MYOSC STANDARD; PRT; 36 AA.

P09641;

01-MAR-1989 (Rel. 10, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

Peptide YY INE (PYY).

Myoxocephalus scorpius (Shorthorn sculpin) (Daddy sculpin).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Actinopterygii; Neopterygii; Percomorpha; Scorpaeniformes;

Octotidei; Cottidae; Myoxocephalus.

NCBI_TaxiD=8097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Pancreas;
MEDLINE-87190954; PubMed=2883025;
Cutfield S.M., Carne A., Cutfield J.F.;
"The amino-acid sequences of sculpin islet somatostatin-28 and peptide YY.";
FEBS Lett. 214:57-61(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
P09476 | P79696 c P79715 c
                                      013253
P79855
P22027
P40141
P28588
P09473
P29204:
Q99123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB 1; Length 36;
Pred. No. 1e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMIDATION.
16F331B73643D7AA CRC64;
                                                                                                                                                                                        ALIGNMENTS
                                       TWHH_DEVPA
TWHH_PUNTE
ATPW_BOVIN
NG4_DROME
LEC3_AXIPO
PYY_LEPSP
PYY_RANRI
RPPA_BPT4
REPA_BPT4
  INS_LEPSP
TWHH_CARAU
                             TWHH_DANKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.5%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hormone, Amidation.
MOD_RES 36
SEQUENCE 36 AA; 4170 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 HAAPED--KYEAFVLHF 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :|:||| || || |:
11 NASPEDWAKYHAAVRHY 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 13.5
Best Local Similarity 52.9
Matches 9; Conservative
 100.8
100.8
100.8
100.8
100.8
100.4
100.4
100.4
100.4
32
32
32
32
31
31
31
31
31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                           PYY_MYOSC

ID PAYLM

AC 01-MA-
DT 01-MA-
DC CC CCLC

CC CCLC

RX MEDLI
RA CULF

RY THE

RY CODI

RY CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PYY_RAJRH
 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db
                                                                                      July 11, 2002, 10:56:12; Search time 10.18 Seconds (without alignments) 216.799 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ornithorhyn
trachemys s
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     felis silve
canis famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synechococc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           balaenopter
camelus dro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    didelphis m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  felis silve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anguilla ro
canis famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dromaius no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            macaca fasc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       xenopus lae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 balaenopter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         capra hircu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    elephas max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oreochromis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    babesia bov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acomys cahi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anser anser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acipenser g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hystrix cri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       petromyzon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vicia faba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               katsuwonus
                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                       SKAPQLVPKLDEVYNAAYNA.....SEALHIIAGTPEVHAVKPGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P42633
P31236
P14806
P14201
P01340
P01324
P07454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P81423
                          Compugen Ltd
                                                                                                                                                                                                                                                                    of hits satisfying chosen parameters:
            GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                           105224 seqs, 38719550 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RK32_VICEA
INS_BALBO
INS_BALBO
INS_CAMDR
INS_CAPHI
INS_CAPHI
INS_INS_ELCA
INS_FELCA
INS_FELCA
INS_FELCA
INS_ACREO
INS_PETWA
INS_ACREO
INS_PETWA
INS_PETWA
INS_PETWA
INS_PETWA
INS_BABBO
INS_RATPE
BABA_BABBO
INS_ARAPE
INS_ARAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYY_RAJRH
PYY_ORENI
ANDP_DROME
OSTC_FELCA
OSTC_CANFA
OSTC_DRONO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OSTC_MACFA
OSTC_RABIT
OSTC_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INS_ANSAN
INS_HYSCR
INS_ORNAN
INS_TRASC
MLEV_MOUSE
INS_ACIGU
                                                                protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                    Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SBK_SYNEL
                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                        Maximum Match 100%
                                                                                                                                             US-09-696-169A-19
297
1 SKAPQLVPKLDEVYNA
                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                              SwissProt_40:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq length: 0
seq length: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perfect score:
                                                                                                                                                                                                  Scoring table:
                                                                  1
                                                                                                                                                                                                                                                                      Total number
                                                                                                                                                                                                                                                                                                 Minimum DB
Maximum DB
                                                                OM protein
                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                            Searched:
                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Result
                                                                                                                                               Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
9
```

ij

```
Hormone; Amidation.
MOD_RES 36
SEQUENCE 36 AA; 4
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                   STRAIN-CANTON-S
                                                                                                                                                             ANDP_DROME
                                                                                                                                                 ANDP_DROME
                                                                                                                                          RESULT
                                                                                                            q
    FT SO
                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                    .;
H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Property of the procedure of the tilapia implications for islet xenograft studies.";

"Comp. Biochem. Physiol. 111C:33-44(1995).

"Comp. Biochem. Physiol. 111C:33-44(1995).

"I. SUBGELLULAR LOCATION: Secreted.

"I. SIMILARITY: BELONGS TO THE NPY / PPY / PYY FAMILY.

RESP: PO1303; IRON.

RIAFS: PRO01955; Pancreatic_hormn.

R Propom; PP001267; Pancreatic_hormn; 1.

R PROSTIE; PS00265; PANCREATIC_HORMONE_1; 1.

R PROSTIE: PS00265; PANCREATIC_HORMONE_2; 1.
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
Cichlidae; Oreochromis.
                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
Rajiformes; Rajidae; Raja
NCBL_TaxID=30478;
                                                                                                                                      2;
                                                                                                                                                                                                                                                                                                                                Length 36;
                                                                                                                                                                                                                                                                                                                                                    6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide YY-like (PYY).
Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
                                                                                                                                                                                                                                                                                        AMIDATION.
07A7D9DC196660B6 CRC64;
                                                                                                                                                                                                                                                                                                                               Score 40; DB 1;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                             01-DEC-1992 (Rel. 24, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Peptide YY-like (PYY).
Raja rhina (Skate).
                                                                                                                                                                                                                                                                                                                                                                                                                                           36 AA.
  36 AA.
                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                        PROSITE: PS00265; PANCREATIC_HORMONE_1; 1. PROSITE; PS50276; PANCREATIC_HORMONE_2; 1.
                                                                                                                                                                                                                           PRINTS; PRO0278; PANCHORMONE.
ProDom; PD001267; Pancreatic_hormn; 1.
SMART; SM00309; PAH; 1.
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95384941; PubMed=7656183;
                                                                                                                              MEDLINE-91296574; PubMed-2067973;
                     (Rel. 24, Created)
                                                                                                                                                                                                                                                                                                                                                                      19 NAADHAAPED--KYEAFVLHF 37
                                                                                                                                                                                                                                                                                                                                                                                         7 NPGDDAAPEELAKYYSALRHY 27
                                                                                                                                                                                                                                                                                                                              13.5%;
42.9%;
                                                                                                                                                                                                                                                                                                 36 AA; 4251 MW;
                                                                                                                                                                                                                                                                                                                                                    9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
  STANDARD;
                                                                                                                                                                                                                                                                                Hormone; Amidation.
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 9; Conserv
                    01-DEC-1992
01-DEC-1992
 PYY_RAJRH
P29206;
                                                                                                                                                                                                                                                                                                                                                                                                                                          PYY_ORENI
P81028;
                                                                                                                                                                                                                                                                                        MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEOUENCE
                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                 PYY_ORENI
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                         g
```

```
Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Holf W., Hoskins R.A., Galle R.F.,
A deams M.D., Celniker S.E., Holf W., Hoskins R.A., Galle R.F.,
A decaye R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A brill J.F., Agbayani A., An H.-J., Andrews-Pfannkohl C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Barman B.P., Bhandari D., Bolshakov S.,
Beeson K.Y., Benos P.V., Berman B.P., Brottier P.,
Borkova D., Botchan M.R., Bulck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Bulter H., Cadleu E., Center A., Chandra I.,
Borkova D., Botchar M.R., Dong Z., Mays A.D., Daw II., Dista S.P.,
A burtis K.C., Busam D.A., Dahlke C., Davenport L.B., Davies P.,
A cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunk D.C.,
Brandin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Rolodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
A larris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wein M.-H., Ibbeyama C.,
A lanktei B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
A Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
A Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
A Martei B., McIntosh T.C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nixon K., Nusskern D.R., Pacleb J.M.,
                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Samakovlis C., Kylsten P., Kimbrell D.A., Engstroem A., Hultmark D., "The andropin gene and its product, a male-specific antibacterial peptide in Drosophila melanogaster."; EMBO J. 10:163-169(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular population genetics of Drosophila immune system genes."; Genetics 147:713-724(1997).
                                                                                                                                                                                                                                     ;
                                                                                                                                                    Score 39; DB 1; Length 36;
Pred. No. 1.4e+02;
2; Mismatches 3; Indels
AMIDATION (BY SIMILARITY).
0246CFBC6243D7AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P21653; 09VA90;
01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-BO09, B141, Z10, Z18, AND Z24; MEDLINE-97476321; Pubmed-9335607; Clark A.G., Wang L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Andropin precursor.
ANP OR ANR OR CG1361.
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=BERKELEY;
MEDLINE=20196006; Pubmed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91114699; PubMed=1899226;
                                                                                                                                                             13.1%;
56.2%;
    36 36
36 AA; 4201 MW;
                                                                                                                                                    Query Match 13.1
Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                             24 AAPED -- KYEAFVLHF 37
                                                                                                                                                                                                                                                                                                                                                          |:||| || || |:
12 ASPEDWAKYHAAVRHY 27
```

```
canine bone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OSTC_CANFA P81455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                   MOD_RES
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOD_RES
MOD_RES
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                MOD_RES
                                                                                                                                                                                                                                                                                                                                           MOD_RES
                                                                                                                                                                                                                                                                                                                                                             MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BGLAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OSTC_CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24
                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Osteocalcin (Gamma-carboxyglutamic acid-containing protein) (Bone Gla-
Palažolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner K., Venter E., Wang A. H., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Yelliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shimomura H., Kanai Y., Sanada K.;
"Primary structure of cat osteocalcin.";
J. Blochem. 96:405-411(1984).
-i- FUNCTION: CONSTITUTES 1-2% OF THE TOTAL BONE PROTEIN. IT BINDS STRONGLY TO APAITE AND CALCIUM.
                                                                                                                                                                                                                                         Science 287:2185-2195(2000).
-!- FUNCTION: MALE-SPECIFIC PEPTIDE WITH MODERATE ACTIVITY AGAINST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39; ....
Pred. No. 2.3e+02;
--+-hes 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.1%; Score 39; DB 1; Length 57;
                                                                                                                                                                                                                                                                                      GRAM-POSITIVE BACTERIA.
-!- TISSUE SPECIFICITY: EJACULATORY DUCT OF ADULT MALES.
-!- INDUCTION: IN RESPONSE TO MATING.
-!- SIMILARITY: STRUCTURALLY RELATED TO CECROPINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEA8CCCF59A09AB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANDROPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=85054706; PubMed=6334077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AF018985; AAB82482.1; --
EMBL, AF018986; AAB82483.1; --
EMBL, AF018989; AAB82486.1; --
EMBL, AF018992; AAB82487.1; --
EMBL, AF018992; AAB82489.1; --
EMBL, AF018992; AAB82489.1; --
EMBL, AF018992; AAB87489.1; --
EMBL, AS003773; AAF57024.1; --
PIR; S13450; S13450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 LDKVENAIHNAAQVGIGFAKPFEK 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 LDEVYNAAYNAAD----HAAPEDK 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insect immunity; Antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X16972; CAA34842.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6151 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase; FBgn0000094; Anp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X56726; CAA40046.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein) (BGP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OSTC_FELCA
P02821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OSTC_FELCA
AC OSTC_FILA
DV 027821-010.
DV 21-010.
DV 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BGLAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

```
Pfam: PF00594; gla: 1.
PRIWES: PR00002; GLABONE.
SMART: SW00069; GLA: 1.
PROSITE: PS00011; GLU_CARBOXXLATION; 1.
Calcium-binding; Gamma-carboxyglutamic acid; Vitamin K; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Osteocalcin (Gamma-carboxyglutamic acid-containing protein) (Bone Gla-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00011, GLU_CARBOXYLATION, 1.
Calcium-binding; Gamma-carboxyglutamic acid; Vitamin K; Hydroxylation;
PTM: GAMMA-CARBOXYGLUTAMIC ACID RESIDUES ARE FORMED BY VITAMIN K DEPENDENT CARBOXYLATION. THESE RESIDUES ARE ESSENTIAL FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Bone Miner. Res. 8:733-743(1993).

-!- FUNCTION: CONSTITUTES 1-2% OF THE TOTAL BONE PROTEIN. IT BINDS STRONGLY TO APATITE AND CALCIUM.

-!- PTM: GAMMA-CARBOXYCLITAMIC ACID RESIDUES ARE FORMED BY VITAMIN DEPENDENT CARBOXYCLATION. THESE RESIDUES ARE ESSENTIAL FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                            BINDING OF CALCIUM.
-!- SIMILARITY: BELONGS TO THE OSTEOCALCIN / MATRIX GLA-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Colombo G., Fanti P., Yao C., Malluche H.H.; "Isolation and complete amino acid sequence of osteocalcin from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE OSTEOCALCIN / MATRIX GLA-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYDROXYLATION (BY SIMILARITY)
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                             GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93D2131FA9F656D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43121D015817CEA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38.5; DB 1;
Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 AA
                                                                                                                                                                                                                                                                                                                                                        HYDROXYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 2.26
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 QLVPKLDEVYNAAYNAADHAAPEDKYEAF 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                     PIR; A03304; GECT.
InterPro; IPR002384; GLA_bone.
InterPro; IPR000294; VitK_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002384; GLA_bone.
InterPro; IPR00294; VitK_dep_GLA.
Pfam; PF00594; gla; l.
PRINTS; PR00002; GLABONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-93318657; PubMed-8101026;
                                                                                                                                                                                                                                                                                                                                                   9
17
21
24
29
5495 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
17
21
24
29
5524 MV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 13.0%;
Best Local Similarity 34.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00069; GLA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BINDING OF CALCIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein) (BGP).
```

÷

```
PIR; A61280; A61280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A03302; GEMKI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 AA;
                                                                                                                               NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OSTC_RABIT
P39056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOD_RES
MOD_RES
MOD_RES
DISULFID
SEQUENCE
                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
OSTC_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Osteccalcin (Gamma-carboxyglutamic acid-containing protein) (Bone Gla-
                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-cocalcin (Gamma-carboxyglutamic acid-containing protein) (Bone Gla-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gla-containing proteins.";
Biochem. Int. 15:271-277(1987).
-!- FUNCTION: CONSTITUTES 1-278
STRONGLY TO APATITE AND CALCIUM.
-!- PTW: GAMMA-CARBOXYGLUTAMIC ACID RESIDUES ARE FORMED BY VITAMIN K
DEPENDENT CARBOXYLATION. THESE RESIDUES ARE ESSENTIAL FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hug N.L., Tseng A., Chapman G.E.; "The amino acid sequence of Emu osteocalcin: gas phase sequencing of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FAMILY.

R PIR; S02208; S02208.

R InterPro; IPR002384; Gita_bone.

DR Pf00594; gla; l.

DR PF00594; gla; l.

DR PROSTIE; PR00002; GLABONE.

SMART; SM00069; GLA; l.

DR PROSTIE; PS00011; GLU_CARBOXYLATION; l.

KW Calcium-binding; Gamma-carboxyglutamic acid; Vitamin K; Bone.

FT MOD_RES 16 GAMMA-CARBOXYGLUTAMIC ACID.

CALCIUM-BES 20 GAMMA-CARBOXYGLUTAMIC ACID.

23 GAMMA-CARBOXYGLUTAMIC ACID.

"OF THE CALCIUM-ACID."

24 CARMA-CARBOXYGLUTAMIC ACID.

CALCIUM-ACID.

CALCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Palaeognathae; Casuariiformes; Dromaiidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE OSTEOCALCIN / MATRIX GLA-PROTEIN
                                                                                                    7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                Length 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 48;
                                                                                                    Indels,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                    .,
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                              Score 37.5; DB 1;
Pred. No. 3e+02;
5; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34.5; DB 1;
Pred. No. 6.8e+02;
4; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                 Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 AA
                                                                                                                                                                                                                                                                                                                                           48
                                                                                                                                                                                      5 QLVPKLDEVYNAAYNAADHAAPEDKYEAF 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 QLVPKLDEVYNAAYNAADHAAPEDKYEAF 33
                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-88134266; PubMed-3501719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dromaius novae-hollandiae (Emu).
                                              12.6%;
31.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.6%;
31.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 31.0°
Matches 9; Conservative
                                                                                                 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BINDING OF CALCIUM
                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=8790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein) (BGP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein) (BGP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OSTC_MACFA P02819;
                                                                                                                                                                                                                                                                                                                                        OSTC_DRONO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dromaius
                                                                                                                                                                                                                                                                                                                                                                      P15504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OSTC_MACFA
                                                                                                                                                                                                                                                                                                                   OSTC_DRONO
                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                      AAC
DDT TO DD TO D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                        õ
```

```
Pfam; PF00051, 91a; 1.
PRINTS; PR00002; GLABONE.
SMART; SM00069; GLA: GLABOXLATION; 1.
Calcium-binding; Gamma-carboxyglutamic acid; Vitamin K; Hydroxylation;
                                                                                                                                                                                                                          Hauschka P.V., Carr S.A., Biemann K.;
"Primary structure of monkey osteocalcin.";
Biochemistry 21:638-642(1982).
-!- FUNCTION. CONSTITUTES 1-25
STRONGLY TO APATITE AND CALCIUM.
-!- PTM: GAMMA-CARBOXYGLUTAMIC ACID RESIDUES ARE FORMED BY VITAMIN K
DEPENDENT CARBOXYLATION. THESE RESIDUES ARE ESSENTIAL FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virdi A.S., Willis A.C., Hauschka P.V., Triffitt J.T.;
"Primary aminoacid sequence of rabbit osteocalcin.";
Biochem. Sco. Trans. 19:373S-373S(1991).
-!- FUNCTION: CONSTITUTES 1-2% OF THE TOTAL BONE PROTEIN. IT BINDS STRONGLY TO APATITE AND CALCIUM.
-!- FPIW: GAMMA-CARBOXYGLUTAMIC ACID RESIDUES ARE FORMED BY VITAMIN PERDINGNY CARBOXYLATION. THESE RESIDUES ARE ESSENTIAL FOR THE BINDING OF CALCIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                           BINDING OF CALCIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -! - SIMILARITY: BELONGS TO THE OSTEOCALCIN / MATRIX GLA-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
05-eccalcin (Gama-carboxyglutamic acid-containing protein)
(Bone Gla-protein) (BGP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34.5; DB 1; Length 49; Pred. No. 7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
C20116014D0C4958 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYDROXYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 ELNPDCDEL-----ADHIGFQEAYRF 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 QLVPKLDEVYNAAYNAADHAAPEDKYEAF 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002384; GLA_bone.
InterPro; IPR000294; Vitk_dep_GLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-92175242; PubMed-1794506;
                                                                                                                                                                                                   MEDLINE-82182842; PubMed-6978733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.6%;
31.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
17
21
24
29
5743 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                         Cercopithecinae; Macaca.
```

ä

```
RK32_VICFA
P15820;
                                                                                                                                                PSBK_SYNEL
                                                                                                                                                                                                                                                                                                                                       Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                           PSBK
                               9
                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
                                                                                           SMARY; SM00069; GLA; 1.
PROSITE; PS00011; GLU_CARBOXYLATION; 1.
Calcium-binding; Gamma-carboxyglutamic acid; Vitamin K; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TC_XENLA STANDARD; PRT; 49 AA.

OSTC_XENLA STANDARD; PRT; 49 AA.

OSTC_XENLA STANDARD; PRT; 49 AA.

OSTC_XENLA STANDARD; PRT; 40 AA.

OSTC_XENLA STANDARD; PRT; 40 AA.

OSTC_XENLA STANDARD; AST SEQUENCE Update)

OSTC_YENLA STANDARD; BONE Glance Carboxyglutamic acid-containing protein) (Bone Glance Standard)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96139691; PubMed=8567186;
Cancela M., Williamson M.K., Price P.A.;
Int. J. Pept. Protein Res. 46:419-423(1995).
-!- FUNCTION: CONSTITUTES 1-2% OF THE TOTAL BONE PROTEIN. IT BINDS
STRONGLY TO APATITE AND CALCIUM.
-!- PTM: GAMMA-CARBOXYGLUTAMIC ACID RESIDUES ARE FORMED BY VITAMIN K
DEPENDENT CARBOXYLLATION. THESE RESIDUES ARE ESSENTIAL FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein) (BGP).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE OSTEOCALCIN / MATRIX GLA-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34.5; DB 1; Length 49;
Pred. No. 7e+02;
4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                              Score 34.5; DB 1; Length 49;
Pred. No. 7e+02;
4; Mismatches 9; Indels
                                                                                                                                                                                         PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Calcium-binding; Gamma-carboxyglutamic acid; Vitamin K; MOD_RES 17 17 CAMMA-CARBOXYGLUTAMIC ACID. MOD_RES 21 21 GAMMA-CARBOXYGLUTAMIC ACID. MOD_RES 22 24 24 CAMMA-CARBOXYGLUTAMIC ACID. DISULFID 23 29 BY SIMILARITY. SEQUENCE 49 AA; 5360 MW; 7A9A8F63A12E6047 CRC64;
                                                                                                                                                                                                                                  GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
BY SIMILARITY.
7B218871F0312253 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00069; GLA; 1.
PROSITE; PS00011; GLU_CARBOXYLATION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 QLVPKLDEVYNAAYNAADHAAPEDKYEAF 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 ELNPDCDEL-----ADQVGLQDAYQRF 45
InterPro; IPR002384; GLA_bone.
InterPro; IPR000294; VitK_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR002384; GLA_bone.
Interpro; IPR00294; VitK_dep_GLA.
Pfam: PF00594; gla; IP
PRINTS; PR00002; GLABONE.
                                                                                                                                                                                                                                                                                                                                                                                                     11.6%;
31.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 31.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                  5431 MW;
                                                                        PRINTS; PR00002; GLABONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                              1
21
24
29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BINDING OF CALCIUM
                                                Pfam; PF00594; gla; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   9;
                                                                                                                                                                                         MOD_RES
MOD_RES
MOD_RES
MOD_RES
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                      Bone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT ON THE PRESCRIPTION OF THE PRESCRIPTION
    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REACTION CENTER PROTEIN K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
MEDLINE=90206803; PubMed=2320425;
Herdenberger F., Pillay D.T.N., Steinmetz A.;
"Sequence of the trnH gene and the inverted repeat structure deletion site of the broad bean chloroplast genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidenosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Vicia
                                                                                                                                                                                                                                                                                                                         Thermosynechococcus elongatus.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE REACTION CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Photosystem II reaction center protein K precursor (PSII-K)
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. Katch H., Ikeuchi M.; "Cloning and disruption of the psbK gene from thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                          ccus elongatus (Thermosynechococcus elongatus).
Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
PHOTOSYSTEM II REACTION
45C5197F4B50E398 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34; DB 1; Pred. No. 7.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1990 (Rel. 14, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Chloroplast 50S ribosomal protein L32.
46 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 AA
                                                                                                                                                                                                                                                                                                                                                                                                                       -! - SIMILARITY: BELONGS TO THE PSBK FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AB052850; BAB20628.1; -.
InterPro; IPR003687; PsbK.
Pfam; PF02533; PsbK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46
5026 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.48;
40.08;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vicia faba (Broad bean).
                                                                                                                                                            Synechococcus elongatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :|| ::| || :|:
DALVLVAKLPEAYAI 17
                                                                                                                                                                                                                                                                                                                                                                                                 OF PHOTOSYSTEM II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 EALHIIAGTPEVHAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46 AA;
                                                                                                                                                                                                          NCBI_TaxID=32046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Photosystem II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chloroplast.
```

ij

Gaps

7;

```
INS_BALPH
P01312:
                                   CHAIN
DISULFID
DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEOUENCE.
                         NON CONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_CONS
                                                                                                                                                                                                                                                                                             Insulin.
                                                                                                                                                                                                                           INS_BALPH
   WTTTTTT
SO
                                                                                                                                                          ò
                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                         Gaps
                   Nature 181:1468-1458(1958).

-!- FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. IT
INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS AND
FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE
CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.

-!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ishihara Y., Saito T., Ito Y., Fujino M.;
"Structure of sperm- and sei-whale insulins and their breakdown by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Balaenoptera borealis (Sei whale).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
Balaenopteridae; Balaenoptera.
NCBI_TaxID=9768;
                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFIDE BONDS.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY
                                                                                                                                                                                                                                                                                                                 11.4%; Score 34; DB 1; Length 48; ilarity 42.9%; Pred. No. 7.9e+02; Conservative 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                     Ribosomal protein; Chloroplast.
SEQUENCE 48 AA; 5407 MW; 146372D6C9BC34DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                         51 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A01582; INWH1S.
HSSP; P01315; 91NS.
InterPro; IPR000739; Insulin_IGF_relaxin.
Wucleic Acids Res. 18:1297-1297(1990).
                                                                                                                                                                                                            PIR: S08495; R5VF32.
PIR: S08444; S08444.
Mendel, 5435; VICEA; VICEA; IPDS: 1.
InterPro; IPR002677; Ribosomal_L32p.
Pfam; PF01783; Ribosomal_L32p; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                                                                                                                         25 YKAALKAFSLADSILTGTSKV 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pfam; PF00049; Insulin; 1.
PR:4TS; PR00276; INSULINA.
PRINTS; PR00277; INSULINB.
SMART; SM00078; IIGF; 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                    EMBL; X51471; CAA35833.1; -.
                                                                                                                                                                                                                                                                                                                                                            30 YEAFVLHFSEALHIIAGTPEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 181:1468-1469(1958)
                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       whale pepsin."
                                                                                                                                                                                                                                                                                                                                                                                                                                        INS_BALBO
P01314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insulin.
                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                             INS_BALBO
 ŏ
                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
ä
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Harris J.I., Sanger F., Naughton M.A.;
"Species differences in insulin.";
Arch Biochem Biochhys. 65:427-438(1956).
-!- FUNCTION: INSULIN DEREASES BLOOD GLUCOSE CONCENTRATION. IT
INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS AND
FATTY ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE
CYCLE, AND GLYCOGEN SYMTHESIS IN LIVER.
-!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES-P. catodon;
Stabihara Y., Saito T., Ito Y., Fujino M.;
"Structure of sperm- and sei-whale insulins and their breakdown by
whale pepsin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Physeter catodon (Sperm whale) (Physeter macrocephalus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
Balaenopteridae; Balaenoptera.
NCBI_TaxID=9770, 9755;
                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Balaenoptera physalus (Finback whale) (Common rorqual), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -:- SUBCELLULAR LOCATION: Secreted.
-:- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
PIR; A91918; INWHF.
PIR; A93142; INWHP.
                                                                                                                                                                                                                                                    Score 34; DB 1; Length 51;
Pred. No. 8.4e+02;
5; Mismatches 6; Indels
                                                                                                                                                                             9007B50E400A7DDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES-B.physalus;
Hama H., Titani K., Sakaki S., Narita K.;
Hama amino acid sequence in fin-whale insulin.";
J. Biochem. 56:285-293(1964).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insulin family; Hormone; Glucose metabolism.
CHAIN 1 30 INSULIN B CHAIN.
Insulin family; Hormone; Glucose metabolism. CHAIN
                                                                            INSULIN A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP, P01315; 91NS.
InterPro; PR000739; Insulin_IGF_relaxin.
Pfan; PF00049; Insulin; 1.
PRINTS; PR00276; INSULINA.
PRINTS; PR00277; INSULINA.
SMARY; SMO0778; IIGF. 1.
PROSITE; PS00262; INSULIN. 1.
                                                                                                      INTERCHAIN.
                                                                                                                           INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                        36 HFSEALHIIAG-----TPEVHAVK 54
                                                                                                                                                                                                                                                                                                                                                                                                        10 HLVEALYLVCGERGFFYTPKAGIVE 34
                                                                                                                                                                                                                                                  11.48;
                                                                                                                                                                             5723 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 181:1468-1469(1958).
                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                               30
31
37
41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFIDE BONDS
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                      19
36
51 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES-P. catodon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PARTIAL SEQUENCE.
```

```
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       dromedarius).";
J. Fac. Med. Baghdad 14:16-28(1972).
J. Fac. Med. Baghdad 14:16-28(1972).
I. Fac. Med. Baghdad 14:16-28 BLOOD GLUCOSE CONCENTRATION. IT INCREASES CELL PERNEABILITY TO MONOSACCHARIDES, AMINO ACIDS AND FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.
-!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                              Camelus dromedarius (Dromedary) (Arabian camel).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
NCBI_TaxID=9838;
                                                                                                                                                                                                                                                                                                                                                                                                            Danho W.O.; The isolation and characterization of insulin of camel (Camelus
                                                                                                                        ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                           11.4%; Score 34; DB 1; Length 51; 32.0%; Pred. No. 8.4e+02; ive 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34; DB 1; Length 51;
Pred. No. 8.4e+02;
5; Mismatches 6; Indels
                                                     9007B514691A7CDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            901E88BA085A7DDD CRC64;
                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INSULIN A CHAIN.
INTERCHAIN.
INTERCHAIN.
    INSULIN A CHAIN. INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INSULIN B CHAIN
                                                                                                                                                                                                                                         51 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A92782; INCMA.
HSSP; P01317; ZINS.
Interpro: IPR000739; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin, 1.
PRINTS; PR00276; INSULINA.
PRINTS; PR00277; INSULINA.
PRINTS; PR00077; INSULINA.
PRINTS; PR00077; INSULINA.
PROSITE; PS00262; INSULINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insulin family; Hormone; Glucose metabolism
                              INTERCHAIN
                                                                                                                                                                                                                                         PRT;
                                                                                                                                              36 HFSEALHIIAG-----TPEVHAVK 54
                                                                                                                                                               36 HFSEALHIIAG-----TPEVHAVK 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 HLVEALYLVCGERGFFYTPKAGIVE 34
  51
37
50
41
5766 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41
5693 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 11.4%;
Best Local Similarity 32.0%;
Matches 8; Conservative
                                                                                          Query Match
Best Local Similarity 32.0
Matches 8; Conservative
                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFIDE BONDS
                           19
36
51 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36
51 AA;
                                       DISULFID
                                                                                                                                                                                                                                      INS_CAMDR
P01320;
               DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_CONS
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                           Insulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
CHA1Ñ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                          INS_CAMDR
                                                                                                                                               ò
                                                                                                                                                                      g
    FFFS
                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

Search completed: July 11, 2002, 10:59:38 Job time: 206 sec

streptomyce sus scrofa sus scrofa

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Database :

```
U92zxl rhizobium m
O16824 drosophila
Q931h2 sulfitor
                                                                                                                                                                                                                                        Owize mouse endog
Office arabidopsis
O92187 helicobacte
O93973 bacillus th
O9656 rhodobacter
O56128 porcine cir
O91861 porcine cir
O91861 porcine cir
O94405 bacillus su
O94405 bacillus su
                                                                                                            Q9umul homo sapien
Q9x8fl streptomyce
Q15456 homo sapien
Q26209 plasmodium
Q26213 plasmodium
Q9n1y7 leishmania
Q9myf astatotilap
                                                                                                                                                                                                   P76096 escherichia
Q9kdc1 bacillus ha
Q45678 bacillus su
Q9lej3 glycine max
                                    Q9ttd6 sus scrofa
Q02801 streptomyce
Q27271 plasmodium
Q92zx1 rhizobium m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alvarenga R., Alves L.M.C., Arruda P., Baia G.S., Baptista C.S., Baroacorsis E.D., Bordin S., Bove J.M., Brinnes M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., A Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., Raga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., A Fraga J.S., Franca E.E., Lambais M.R., Latelina J.P., Krieger J.E., Kltajima J.P., Krieger J.E., Mardeira A.M.B.N., Madeira M.C., Marino C.L., Mardeira A.M.B.N., Madeira H.M.F., Marsuck M.Y., Mardeira A.M.B.N., Madeira H.M.F., Marsuck M. Marques M.V., Mardeira A.M.B.N., Madeira M.R., Marsuck M. Marques M.V., Mardeira A.M.B.N., Madeira H.M.F., Marsuck M. Marques M.V., Mardeira A.M.B.N., Madeira M.R., Marsuck M.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                         018822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 AA
                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                           O9R656
O56128
O91861
                                                           Q27271
Q922X1
                                                                                   016824
0931H2
0938H1
0938R1
0915456
026219
026219
09NLY
09NLY
09NLZ
09NLZ
09NLZ
09NLZ
09NLZ
09NLZ
09NLZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                      018822
Q9TTD6
Q02801
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20365717; PubMed=10910347;
252220052
                                                                                                                                       09PA18;
01-0CT-2000 (TrEMBLrel. 15,
01-0CT-2000 (TrEMBLrel. 15,
01-DEC-2001 (TrEMBLrel. 19,
HYPOTHETICAL PROTEIN XF2529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xylella fastidiosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Xylella.
NCBI_TaxID=2371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-9A5C
Q9PAI8
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9PAI8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9pai8 xylella fas Q9lej5 glycine max Q9le39 glycine max Q9pdu4 xylella fas Q9vq65 drosophila O61654 ceratitis c Q9uqy8 colletotric Q9uqy8 colletotric Q9uqy8 colletotric Q9rid3 yersinia pe Q9v779 drosophila Q9mys2 cryctolagus Q9ig77 chilo iride Q9k777 bacillus ha
                                                                            July 11, 2002, 10:55:52; Search time 24.05 Seconds (without alignments) 410.009 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O16823 drosophila
Q9pej8 xylella fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                            1 SKAPQLVPKLDEVYNAAYNA.....SEALHIIAGTPEVHAVKPGA
          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                            562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                            - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                          summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9LEJ5
Q9LE39
Q9PDU4
Q9VQ65
061654
Q9UQY8
Q9APQ5
Q9RID3
Q9V779
                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9MYS2
Q91G77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9PAI8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                      sp_fungi:*
sp_human:*
sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_organelle:*
sp_phage:*
                                                                                                                                     US-09-696-169A-19
                                                                                                                                                                                                                                                                                                                                                                SPTREMBL_19:*
.: sp_archea:*
.: sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100
110
110
110
110
110
110
110
                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                          sb_mhc:*
                                                                                                                                                                                                                                                                           Minimum DB seq length: 0 Maximum DB seq length: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
```

Q9PEJ8

Score 45.5

Result

```
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
                                                                                                                                                                                                                                                                   Query Match 14.8
Best Local Similarity 31.6
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xylella fastidiosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                        SEQUENCE FROM N.A.
                                                                                                     SEQUENCE FROM N.A.
                                                     STRAIN-CV. CLARK;
Vodkin L.O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xylella.
NCBI_TaxID=2371;
               NCBI_TaxID=3847;
                                                                                                                                                                                                                   NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                       O9PDU4;
                                                                                                                                                                                                                                                                                                                                                                                                             Q9PDU4
                                                                                                                                                                                                                                                                                                                                                                                    RESULT
Q9PDU4
                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                        QY
                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                     Glycine max (Soybean).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bermatophyta; Magnaliophyta; eudicotyledons; core eudicots; Rosidae;
Spermatophyta; Magnaliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papliionoideae; Phaseoleae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glýcine max (Soybean).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatopwyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stromvik M.V., Sundararaman V.P., Vodkin L.O.;
"A novel promoter that is active in a complex developmental pattern with and without its proximal 650 base pairs.";
Plant Mol. Biol. 41:217-231(1999).
EMBL; AJ293440; CAB96762.1; -.
da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A., de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H., Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L., Zago M.A., Zatz M., Maidanis J., Setubal J.C., "The genome sequence of the plant pathogen Xylella fastidiosa."; "The genome sequence of the plant pathogen Xylella fastidiosa."; Mature 406:151-159(2000).

EMBL; ABC04060; AAF85327.1; -: Hypothetical protein; Complete proteome.

SEQUENCE 54 AA; 5931 MW; 25524B5C5018E13F CRC64;
                                                                                                                                                                    ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
80
                                                                                                                                          Score 45.5; DB 16; Length 54; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB 10; Length 42;
Pred. No. 2e+02;
6; Mismatches 12; Indels
                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 AA; 4935 MW; 2327B258B8A2CFA5 CRC64;
                                                                                                                                                                                            26
                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MAJQR LATEX PROTEIN HOMOLOGUE (FRAGMENT).
                                                                                                                                                                                                          2 NNPSNEKHHTTPPLELSDECVSNFSELIKALAAYKEINAKKKG
                                                                                                                                                                 7; Mismatches 22;
                                                                                                                                                                                          15 NAAYNAADHAAPE-DKYEAFVLHFSEALHIIAGTPEVHAVKPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 YEKVDHTAPEPTKYKDLVVKLTKNV-----EAHLVE 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54
                                                                                                                                                                                                                                                                                  42 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 YNAADHAAPE-DKYEAFVLHFSEALHIIAGTPEVHAVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Mismatches
                                                                                                                                                                                                                                                                                                                                             MAJOR LATEX PROTEIN HOMOLOGUE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-CV. CLARK;
MEDLINE-20044090; PubMed-10579489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.8%;
                                                                                                                                          15.3%;
                                                                                                                                       Query Match 15.39
Best Local Similarity 30.29
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CV. CLARK;
Vodkin L.O.;
                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3847;
                                                                                                                                                                                                                                                                                                         01-OCT-2000
                                                                                                                                                                                                                                                                                                                    01-OCT-2000
                                                                                                                                                                                                                                                                                                                                  01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9LE39;
Q9LE39;
                                                                                                                                                                                                                                                                                           09LEJ5;
                                                                                                                                                                                                                                                                                Q9LEJS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                     Q9LEJ5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9LE39
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
Alughorn A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alucinear A.J.G., Reinach F.C., Arruda D., Baid G.S., Baptista C.S., Ratarosa M.H., Bonacororsi E.D., Bordin S., Bove J.M., Erlones M.R.S., Bueno M.R.P., Camargo L.E.A., Carraro D.M., Carrer H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., R. Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., R. Franca S.C., Franca S.C., Franca S.C., Franca S.C., Franca W.C. R. Forlan L.R., Rata J.S., Ferreira V.C.A., Ferro J.A., Rata Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A., R. Krieger J.E., Kuramae E.E., Langstet F., Lambais M.R., Leite L.C.C., Lemos M.V.F., Lopes C.R., Machado J.A., Marques M.W., Martins E.M.E., Martins E.M.F., Martins M.A., Martins M.A., Martins E.M.F., Martins M.A., Martins M.A., Martins E.M.F., Martins M.A., Martins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                           Stromvik M.V., Sundararaman V.P., Vodkin L.O.;
"A novel promoter that is active in a complex developmental pattern with and without its proximal 650 base pairs.";
Plant Mol. Biol. 41:217-231(1999).
EMBL; AJ293442; CAB967661;
-..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45 AA; 5236 MW; 2327E24CEA15458E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL PROTEIN XF1285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.8%; Score 44; DB 10;
31.6%; Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 YNAADHAAPE-DKYEAFVLHFSEALHIIAGTPEVHAVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26
                                                                                                                                         STRAIN=CV. CLARK;
MEDLINE=20044090; Pubmed=10579489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20365717; PubMed-10910347;
```

5

us-09-696-169a-19.closed.rspt

```
Flybase; FBgn0040718; CG15353.
SEQUENCE 53 AA; 5450 MW; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glomerella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                               Query Match
                                                                                                                                                                                                                           061654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09UQY8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9UQY8
                                                                                                                                                                                                RESULT
O61654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9UQY8
    SO
                                                                                                                         δy
                                                                                                                                                  g
                                                                                                                                                                                                                                            δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Suddence From N.A.

RY STRAIN-BERKELEY.

RY MEDLINE-20196006; PubMed=10731132;

RAdans W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adans W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adans W.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.M.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Brandon R.C., Rogars Y.H.C., Bazel F.G., Champe M., Pefelffer B.D.,

RA Brandon R.C., Rogars Y.H.C., Bazel F.G., Champe M., Pefelffer B.D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Cawley S., Dahlke C., Barckstein D., Botshakov S.,

RA Ballew R.M., Cawley S., Dahlke C., Davenport L.B., Davice P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davice P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davice P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davice P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davice P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davice P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davice P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davice P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davice P.,

RA Godek A., Gong F. C., Ferrac C., Ferrac C., Ferrac S.,

RA Godek M., Marvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Harris B., McIncosh T.C., McLeod M.P., McBroon D.R.,

Relazon D.R., Melson K.A., Mixon K., Nusskern D.R., Melson D.R.,

RA Plazzolo M., Pittman G.S., Pan S., Pollard J., Puil V.,

RA Plazzolo M., Pittman G.S., Pan S., Pollard J., Puil V., Wang X.,

RA Shue B.C., Stden-Kiamos I., Simpson M., Strong R., Sun R.,

RA Shue B.C., Spradling A.C., Saunders R.D.C., Scheeler F., Shen H.,

RA Shen S.M., Woodage T.W., Wooley K.C., Wu D., Yang 
                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                        Gaps
"The Jenome sequence of the plant pathogen Xylella fastidiosa."; Nature 406:151-159(2000). EMBL; AE003962; AAF84094.1; -.
                                                                                                                                       ö
                                                                                                        Length 56;
                                                                                                                                       Indels
                                           Hypothetical protein; Complete proteome.
SEQUENCE 56 AA; 6500 MW; 58D8C85B0B116BF4 CRC64;
                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                     16;
                                                                                                        14.8%; Score 44; DB 16; 25.7%; Pred. No. 2.8e+02; Live 10; Mismatches 16
                                                                                                                                                                                                                                                                        53 AA.
                                                                                                                                                                                      8 PKLDEVYNAAYNAADHAAPEDKYEAFVLHFSEALH 42
                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                      Best_Local Similarity 25.79
Matches 9; Conservative
                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                CG15353 PROTEIN
                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                               CG15353
                                                                                                                                                                                                                                                                      090065
                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                        09VQ65
 RE DR XX
                                                                                                                                                                   ò
```

```
1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=M5.001, AND M1.001;
STRAIN=M5.001, AND M1.001;
Valilancourt L.J.; Du M., Wang J., Rollins J., Hanau R.;
"Genetic analysis of cross-fertility between two self-sterile strains of Glomerella graminicola.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF204961; AAF23399.1;
EMBL; AF204960; AAF23399.1;
                                                                                                                                                                                                                                                                                                                                                                       UI-DEC-2001 (TrEMBLrel. 19, Last sequence update)
CYTCCHROME P450 MONOCXYGENASE (FRAGMENT).
Ceratitis capitata (Mediterranean fruit fly).
Eukartyota; Medazoa: Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
NCBL_TaxID=7213;
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
                                                                                                                  5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 17, Last annotation update)
PUTATIVE MAY-2 MATING TYPE PROTEIN (FRACHENT).
Colletotrichum graminicola (Anthracnose fungus) (Glomerella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Danielson P.B., Foster J.L.M., Cooper S.K., Fogleman J.C.;
Danielson P.B., Foster J.L.M., Cooper S.K., Fogleman J.C.;
"Diversity of Expressed cytochrome P450 Genes in the Adult Mediterranean Fruit Fly, Ceratitis capitata.";
Submitted (APR.1998) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AF056473; AAC13306.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 43; DB 5; Length 50, Pred. No. 3.7e+02;
                                                                      Length 53;
663595A2F81D2E9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6274 MW; 28B0EE6F10415A27 CRC64;
                                              Score 43; DB 5; Ler
Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                56 AA
                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heme; Monooxygenase; Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                              1 SKAPQLVPKLDEVYNAAYNAADHAAP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001128; Cyt_P450.
Pfam; PF00067; p450; 1.
                                                                 14.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.58;
44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | | |:|||: ::|:|
32 EMKLESFVLNSKDGIHLI 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 EDKYEAFVLHFSEALHII 44
                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
'-hes 8; Conserv?
                                                                                          Best Local Similarity
Matches 11; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=31870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     graminicola).
```

```
CG12853
                                                                                                                                                                                                                   097779;
                                                                                                                                                                                                          09V779
                                                                                                                                                                                        RESULT 10
                                                                                                                                                                                                  09V779
     g
                                                                                                                                          ò
                                                                                                                                                                                                                             ö
                                                                                         3
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                          Gaps
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=2075196; PubMed=11133432;
Entcheva P., Liebl W., Johann A., Hartsch T., Streit W.R.;
Entcheva P., Liebl W., Johann A., Hartsch T., Streit W.R.;
"Direct cloning from enrichment cultures, a reliable strategy for isolation of complete operons and genes from microbial consortia.";
Appl. Environ. Microbiol. 67:89-99(2001).

EMBL; AF250771; AAG60565.1; -.

NON_TER 44 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacterla; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                          5;
                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 2; Length 44; Pred. No. 5e+02;
                                                                      Score 42; DB 3; Length 56
                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                             11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CO-92 BIOVAR ORIENTALIS;
Baker S.G., Mungall K.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           James K.D., Parkhill J., Barrell B.G., Rajandream M.A., Submitted, (SEP-1999) to the EMBL/GenBank/DDBJ databases
                                         B2BBA04C95819EAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                6C73B171FDE4F678 CRC64;
                                                                                                                                                                                     Q9APQ5;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MXY-2000 (TrEWBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 5.4 KDA PROTEIN.
                                                                                         17;
                                                                  14.1%; Score 4.4, ___ 32.4%; Pred. No. 5e+02; +ive 6; Mismatches
                                                                                                           4 POLVPK-LDEVYNAAYNAADHAAPEDKYEAFVLHFSE 39
                                                                                                                       48 AA.
                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                 11 DEVYNAAYNAADHAAPEDKYEAFV 34
                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; environmental samples. NCBI_TaxID=143796;
InterPro; IPR000910; HMG_12_box.
Pfam; PF00505; HMG_box; 1.
NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-CO-92 BIOVAR ORIENTALIS;
                                                                                                                                                                                                                                                                                                                                                                                           13.8%;
37.5%;
                                         6688 MW;
                                                                                                                                                                                                                                               uncultured bacterium pCosHE1
                                                                                                                                                                                                                                                                                                                                                                44 AA; 5262 MW;
                                                                                                                                                                                                                                                                                                                                                                                           Query Match 13.89
Best Local Similarity 37.55
Matches 9; Conservative
                                                                                        12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                             PRELIMINARY;
                                                                      Query Match
Best Local Similarity
                                         56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YMT1.42AC.
Yersinia pestis.
                                                                                                                                                                                                                             ELSG (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pMT1
                               NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                      NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ersinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9RID3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9RID3
                                                                                                                                                                            09APQ5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               σ
                                                                                                                                                          æ
                                                                                        Matches
                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                    09APQ5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9RID3
   DR
FT
SO
                                                                                                           ò
                                                                                                                                                                                       g
                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
```

```
RC STRAIN—EBERKELEY.

RX MEDLINE-20196006; PubMed=10731132;

RR Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,

RA Gucton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Abril J.E., Agbayani A., An H.-J., Andrews-Frankoch C., Baladwin D.,

RA Abril J.E., Agbayani A., An H.-J., Andrews-Frankoch C., Baladwin D.,

RA Beeson K.Y. Basu A., Baxendale J., Barkaktaroll L., Beasley E.M.,

RA Beeson K.Y. Banos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Eusam D.A., Buller H., Cadleu E., Center A., Chandra I.,

RA Berry J.M., Cawley S., Dallike C., Davenport L.B., Davies P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein D., Bolshakov S.,

Borkova D., Botchan M.R., Bouck J., Brokstein D., Bolshakov S.,

RA Godek A., Gong F. Gorrell J. H., Gu Z., Guan P., Harris M.,

RA Hostin D., Houston K.A., Helman T.J., Weinander J.R., Honck J.,

RA Hostin D., Houston K.A., Howland T.J., Weinander J.R., Holler M. A.

Alalli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.

Alalli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Metrei B., McIntosh T.C., McLeod M.P., McIntosh T.C.,

RA Merkilov G. Milshina N.V., Mobarry C., Morris J., Worsheel J.A.,

RA Mestellor R.M., Murphy B., Murphy L., Murany D.M., Nelson D.K.,

RA Bazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Wang S., Nan B.,

Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Syriskas R., Tector C., Turner R., Venter E., Wang A., Wang P., Wang 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pherygota, Neoptera, Endopherygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                            Query Match 13.8%; Score 41; DB 2; Length 48; Best Local Similarity 31.4%; Pred. No. 5.6e+02; Matches 11; Conservative 5; Mismatches 19; Indels
SEQUENCE FROM N.A.
STRAIN=CO-92 BIOVAR ORIENTALIS;
Karlyshev A.V., Wren B.W.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ALI17211; CAB62369.1;
Hypochetical protein; Plasmid.
SEQUENCE 48 AA; 5417 MW; BFD2188AF24BED48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 LDEVYNAAYNAADHAAPEDKYEAFVLHFSEALHII 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CG12853 PROTEIN.
```

ô

```
EMBL; AJ297379; CAB96070.1;
HSSP; P04475; 1DKY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                              54 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in mice.";
                                          NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Darai G
                                                                                                                                                                                                                                                                                                                                                                                 091677;
                                                                                                                                                                                                                                                                                                                                                             Q91G77
                                                                                                                                                                                                                                                                                                                      RESULT 13
                                                                                                                                                                                                                                                                                                                                           091G77
        DR
DR
FT
SQ
                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                 HANDER HER BERKER BERKERE BERKER 
                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna. NCBI_TaxID=3917;
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-NEW ZEALAND; TISSUE-BLOOD;
Rogel-Gaillard C., Plumi F., Billault A., Bourgeaux N., Save J.C.,
Orien C., Salmon J., Chardon P.;
"Construction of a rabbit bacterial artificial chromosome (BAC)
library: application to the mapping of the major histocompatibility
complex to position 12q1.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vigna unguiculata (Cówpea).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Partial genomic nucleotide sequence of a glutelin 2 (gamma zein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 56;
                                                                                                                                     Score 40; DB 5; Length 54; Pred. No. 8.5e+02; 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homolog from cowpea (Vigna unguiculata).";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AF142332; AAD34914.1;
                                    EMBL; AE003812; AAF58180.1; -.
FlyBase; FBgn0040747; CG12853.
SEQUENCE 5,4 AA; 5319 MW; DDDC6742335E8BAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D79613A9F8B84C08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
"Th2 genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39.5; DB 10;
Pred. No. 1e+03;
4; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                           56 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 PEDKYEAFVLHFSEALHIIAGTPE-VHAVKPG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 PEPVHIPEPVHI-----PEPVHIPEPG 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEAT SHOCK PROTEIN 70 (FRAGMENT).
                                                                                                                                                                           3;
                                                                                                                                                                                                                 8 PKLDEVYNAAYNAADHAAPEDK 29
                                                                                                                                                                                                                                        23 PTADPVTSESNNAAEPAAKEAK 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.3%; fullarity 37.5%; fonservative 4;
                                                                                                                                     13.5%;
                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6233 MW;
                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel, 12, (TrEMBLrel, 12,
                                                                                                                               Query Match 13.5
Best Local Similarity 45.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLUTELIN 2 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CV. IT84E-124;
Machuka J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56
56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                           Q9XFG5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSP70-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9MYS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09MYS2
                                                                                                                                                                                                                                                                                                                RESULT 11
Q9XFG5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ď
                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
```

```
MEDLINE=9118242; PubMed=1475907; Sonntag K.C., Darai G.; Characterization of the third origin of DNA replication of the genome of insect inidescent virus type 6.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=89073752; PubMed=3201750;
Fischer M., Schnitzler P., Delius H., Darai G.;
"Identification and characterization of the repetitive DNA element in the genome of insect iridescent virus type 6.";
Virology 167:485-496(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular cloning and physical mapping of the genome of insect
biddescent virus type 6: further evidence for circular permutation of
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=86174607; PubMed=3959991;
Lorbacher de Ruiz H., Gelderblom H., Hofmann W., Darai G.;
"Insect iridescent virus type 6 induced toxic degenerative hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Identification and mapping of origins of DNA replication within the DNA sequences of the genome of insect iridescent virus type 6."; Virus Genes 6:19-32(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-92196996; PubMed-1549908;
Handermann M., Schnitzler P., Rosen-Wolff A., Raab K., Sonntag K.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Delius H., Darai G., Fluegel R.M.;
"DNA analysis of insect iridescent virus 6: evidence for circular permutation and terminal redundancy.";
J. Virol. 49:609-614(1984).
                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chilo iridescent virus (CIV) (Insect iridescent virus type 6). Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus NCBI_TaxID=10488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-87321126; PubMed-2820141;
Schnitzler P., Soltau J.B., Fischer M., Reisner H., Scholz J.,
Delius H., Darai G.;
                                                                                             Score 39; DB 6; Length 54;
Pred. No. 1.1e+03;
6; Mismatches 13; Indels
      44630BD1963DF3E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Med. Microbiol. Immunol. 175:43-53(1986).
                                                                                                                                                                                                                                                                  23 APRGVPQIEVTFDIDANGILHVTATDK 49
                                                                                                                                                                                                                           3 APQLVPKLDEVYNAAYNAADHAAPEDK 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                13.18;
29.68;
5748 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Virus Genes 6:333-342(1992)
                                                                                             Query Match 13.1
Best Local Similarity 29.6
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the viral genome.";
Virology 160:66-74(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
```

DE0A2E74201055F9 CRC64;

us-09-696-169a-19.closed.rspt

```
56 AA; 7186 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANP OR CG1361.
   SEOUENCE
                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANDROPIN
                                                                                                                                                                                                                   Q9K7C7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    016823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    016823
                                                                                                                                                                                                       Q9K7C7
                                                                                                                                                                                                                                                                                              BH3437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       016823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S
                                                                                                                                                                                                         ŏ
                                                                                                     ò
                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-21342589; PubMed-11448171;
Jakob N.J., Muller K., Bahr U., Darai G.;
"Analysis of the First Complete DNA Sequence of an Invertebrate
Iridovirus: Coding Strategy of the Genome of Chilo Iridescent Virus.";
Virology 286:182-196(2001).
                                                                                                                                            "Identification of genes encoding zinc finger proteins, non-histone chromosomal HMG protein homologue, and a putative GTP phosphohydrolase in the genome of Chilo iridescent virus."; Nucleic Acids Res. 22:158-166(1994).
                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-9453541; PubMed-8073636; MEDLINE-9453541; PubMed-8073636; Sonntag K.C., Schnitzler P., Koonin E.V., Darai G.; Sonntag K.C., Schnitzler P., Koonin E.V., Darai G.; "Chilo iridescent virus encodes a putative helicase belonging to a distinct family within the 'DEAD/H' superfamily: implications for the evolution of large DNA viruses."; virus Genes 8:151-158(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-94292906; PubMed-8021587; Schnitzler P., Sonntag K.C., Muller M., Janssen W., Bugert J.J., Koonin E.V., Dazal G.; Insect irridescent virus type 6 encodes a polypeptide related to the largest subunit of eukaryotic RNA polymerase II."; J. Gen. Virol. 75:1557-1567(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98141693; PubMed=9482589;
Bahr U., Tidona C.A., Darai G.;
"The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101 and 0.391; similarities in coding strategy between insect and vertebrate iridoviruses."; virus Genes 15:235-245(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99383793; PubMed=10456793; Muller K., Tidona C.A., Darah G.; "Lidentification of a gene cluster within the genome of Chilo iridescent virus encoding enzymes involved in viral DNA replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99125223; PubMed=9926400;
Muller K., Tidona C.A., Bahr U., Darai G.;
"Identification of a thymidylate synthase gene within the genome of
                                                                                                                                                                                                                                                                                                                                                                                    of
             Stohwasser R., Raab K., Schnitzler P., Janssen W., Darai G.; "Identification of the gene encoding the major capsid protein of insect iridescent virus type 6 by polymerase chain reaction."; J. Gen. Virol. 74:873-879(1993).
                                                                                                                                                                                                                                                                                                                                                                                  capacity
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-95213160; PubMed-7698884;
MEDLINE-95213160; PubMed-7698884;
Sonntag K.C., Schnitzler P., Janssen W., Darai G.;
"Identification of the primary structure and the coding capacity the genome of insect iridescent virus type 6 between the genome coordinates 0.310 and 0.347 (7990 bp).";
Intervirology 37:287-297(1994).
                                                                                                  MEDLINE-94167241; PubMed-8121799;
Schnitzler P., Hug M., Handermann M., Janssen W., Koonin E.V.,
Delius H., Darai C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Jakob N.J., Muellor K., Bahr U., Darai G.;
Submitted (SFP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF303741; AAK81955.1; -
MEDLINE=93260401; PubMed=8492091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virus Genes 17:243-258(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virus Genes 18:243-264(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chilo iridescent virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and processing."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12]
```

```
ö
                                         ς,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoda, Arthropoda, Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clark A.G., Wang L.;
"Molecular population genetics of Drosophila immune system genes.";
Genetics 147:713-724(1997).
EMBL; AF018988; AAB82485.1; -.
FLYBASE; FBGN0000094; ARP.
SEQUENCE 57 AA; 6185 MW; F2C57A0859B839B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S., Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                           ;
6
  Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2CFE84E462446B3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
NCBL_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
Score 39; DB 12; I
Pred. No. 1.2e+03;
8; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB 16;
Pred. No. 1.2e+03;
                                                                                                                                                                                                                                   56 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1.26
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57
                                                                                  19 NAADHAAPEDKYEAF----VLH-FSEALHI 43
                                                                                                                         46
                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20512582; PubMed=11058132;
                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-B316;
MEDLINE-97476321; PubMed-9335607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||||||| : : 17 LDEVYNGGRRPAYHPKMMTKIQLY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 LDEVYNAAYNAADHAAPEDKYEAF 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6569 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 13.1%;
Best Local Similarity 37.5%;
Matches 9; Conservative
  13.1%;
25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05,
05,
16,
                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15,
                                           Conservative
                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
GTDATN-C-125 / JCM 9153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1998 (TrEMBLrel. 01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                Bacillus halodurans.
                     Best_Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                      BH3437 PROTEIN.
```

```
      Query Match.
      13.1%; Score 39; DB 5; Length 57;

      Best Local Similarity 45.8%; Pred: No. 1.2e+03;
      45.6%; Pred: No. 1.2e+03;

      Matches 11; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

      Qy 10 LDEVINAAVINAD----HAAPEDK 29

      ||:|||||||

      Db 29 LDKVENAINAAQVGVGFAKPFEK 52
```

Search completed: July 11, 2002, 10:59:22 Job time: 210 sec **7** 

```
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                              Sequence
Sequence
Sequence
                                                                                                                                                                                   Sequence
Sequence
Sequence
                                         Sequence
                                                      Sequence
                            Sequence
                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 65; DB 1; Length 20;
Pred. No. 0.023;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Griffith, Irwin J.
APPLICANT: Kuo, Mei-Chang
APPLICANT: Luqman, Mohammad
TITLE OF INVENTION: T CELL EPITOPES OF RYEGRASS POLLEN
TITLE OF INVENTION: ALLERGEN
CORRESPONDENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE 6 COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILLIG DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,016
FILING DATE: 31-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 1PC-075 (IMI-040CP)
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
         US-08-488-351A-37
US-08-433-854-23
US-08-433-854-25
US-08-174-745A-25
US-08-174-75A-25
US-08-195-947-23
US-08-433-885-23
US-08-433-908B-23
US-08-433-908B-25
US-08-433-908B-25
US-08-413-908B-25
US-08-410-614-23
US-08-410-614-23
US-08-423-646A-66
                                                                                                                                                                                                                          US-08-471-052A-45
                                                                                                                                                                                                            US-08-176-500-45
                                                                                                                                                                                               US-09-099-307-3
                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: LAHIVE & COCKFIELD 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCII: Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,861
FILING DATE: 15-MX-1995
CLASSIFTCATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/08440861
Patent No. 5710126
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.9%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-440-861-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                         RESULT 1
US-08-440-861-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY:
Sequence 21, Appl
Sequence 7, Appli
Sequence 6, Appli
Sequence 3, Appli
                                                                                     July 11, 2002, 10:52:37; Search time 12.96 Seconds (without alignments) 107.427 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1226, Ap
Sequence 1226, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14,
Sequence 28,
Sequence 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15,
Sequence 10,
Sequence 8, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, 1
Sequence 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 28,
Sequence 28,
                                                                                                                                                                    1 SKAPQLVPKLDEVYNAAYNA......SEALHIIAGTPEVHAVKPGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-817-926-3
US-09-082-279B-1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-315-304B-1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08 440-861-13
US-08 440-861-14
US-08 43-854-28
US-08-195-947-28
US-08-195-947-28
US-08-433-985-28
US-08-433-908-28
US-08-440-861-15
US-08-440-861-10
US-08-440-861-10
US-08-440-861-10
US-08-440-861-10
US-08-214-770-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-440-861-8
US-08-963-851-9
US-08-905-574-4
US-08-440-861-7
US-08-749-861-7
US-08-749-526-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-082-279B-784
US-09-315-304B-784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-963-851-10
US-08-936-165A-365
                                                                                                                                                                                                                                                             hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-440-861-12
                                                                                                                                                                                                                                      231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                               protein - protein search, using sw model
                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                         US-09-696-169A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                      length: 0
length: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match
                                                                                                                                                                                                                                                             Total number of
                                                                                                                                                                                                                                                                                         sed
                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.5
38.39
38.38
38
37
37
                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41
```

Minimum DB s Maximum DB s

Sequence:

Run on:

ĕ

Database :

Result

Š.

ö

Gaps

ö

QQ δ

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.9%; Score 56; DB 1; Length 20; 55.0%; Pred. No. 0.36;
                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/440,861
FILING DATE: 15-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/106,016
FILING DATE: 31-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: AMY E. MANCAGOUTAS
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 16C-075 (IMI-040CP)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                   E: LAHIVE & COCKFIELD
60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,861
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 AAPEDKYEAFVLHFSEALHI 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 55.0
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASCII Text
CORRESPONDENCE ADDRESS:
                                                                      Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                    Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: US
                                                                                                           02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-440-861-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-440-861-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                            Sequence 11, Application US/08440861

Patent No. 5710126

GENERAL INFORMATION:
APPLICANT: GLIFATH, Irwin J.
APPLICANT: Kuo, Mei-Chang
APPLICANT: Lugman, Mohammad
TITLE OF INVENTION: ALLERGEN
TITLE OF INVENTION: ALLERGEN
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHITVE & COCKFIELD
STREET: 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T CELL EPITOPES OF RYEGRASS POLLEN ALLERGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

SOFTWARE: ACCII Text
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/440,861
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,016
FILING DATE: 31-AUG-1993
ATTORNEY/ACENT INFORMATION:
NAME: AND E. MANDERS: 1PC-075 (IMI-040CP)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TTYPE: amino acids
TTYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 62; DB 1;
Pred. No. 0.057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/08440861
Patent No. 5710126
GENERAL INFORMATION:
APPLICANT: Griffith, Irwin J.
APPLICANT: Kuo, Mei-Chang
APPLICANT: Luqman, Mohammad
APPLICANT: Luqman, Mohammad
TITLE OF INVENTION: T CELL EPITOPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.9%;
57.9%;
               14 YNAAYNAADHAAPEDKYEAF 33
                                     4 PQLVPKLDEVYNAAYNAAD 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 20.9
Best Local Similarity 57.9
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-440-861-11
                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                   02109
                                                                                                           RESULT 2
US-08-440-861-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
US-08-440-861-13
```

ò

ö

Gaps

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5736362ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.2%; Score 48; DB 1; Length 13; 83.3%; Pred. No. 2.4; tive 0; Mismatches 2; Indels
                                                                                                         Length 13;
                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 19103

COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/174,745A
                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ong, Eng Kok
TITLE OF INVENTION: Ryegrass Pollen Allergen
MWBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                       Score 48; DB 1;
Pred. No. 2.4;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,7112
REFERENCE/DOCKET NUMBER: IMPH-0024
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Singh, Mohan Bir
APPLICANT: Knox, Robert B.
APPLICANT: Smith, Penelope
APPLICANT: Avjioglu, Asil
APPLICANT: Theerakulpisut, Piyada
APPLICANT: Suphioglu, Cenk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,060
FILING DATE: 14-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                          RESULT 6
US-08-174-745A-28
US-08-174-745A-28
Sequence 28, Application US/08174745A
Patent No. 5736362
GENERAL INFORMATION:
                                                                                                   16.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEO ID NO: 28
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 amino acids
                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 83.3
Matches 10; Conservative
  ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-433-854-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide US-08-174-745A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                           44 IAGTPEVHAVKP 55
                                                                                                                                                                                                                                1 IAGALEVHAVKP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 IAGTPEVHAVKP 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IAGALEVHAVKP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                       Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                  a
                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5721119ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                  18.2%; Score 54; DB 1; Length 20; 60.0%; Pred. No. 0.66; tive 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Knox, Robert B.
APPLICANT: Smith, Penelope
APPLICANT: Swith, Pall
APPLICANT: Avjioglu, Asil
APPLICANT: Hough, Terryn
APPLICANT: Suphioglu, Cenk
APPLICANT: Suphioglu, Cenk
APPLICANT: Or Suphioglu, Ryegrass Pollen Allergen
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                        NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IPC-075 (IMI-040cp)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: HOLDERCHUEZ, LIZA D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: IMPH-0024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
US 08/106,016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ús 07/930,060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/433,85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Singh, Mohan Bir
APPLICANT: Knox, Robert B.
APPLICANT: Smith, Penelope
APPLICANT: Avjioglu, Asil
APPLICANT: Theerakulpisut, Piyada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 28, Application US/08433854 Patent No. 5721119 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 VLHFSEALHIIAGTPEVHAV 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 31-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 14 ANG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 60.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 13 amino acids TYPE: amino acid
                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLGGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-440-861-14
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
US-08-433-854-28,
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
```

ó

```
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Lahive & Cockfield, LLP STREET: 28 State Street
                                                                                                                                       ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 28, Application US/08433908B Patent No. 5965455 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 16.2%;
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: peptide US-08-433-885-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IAGALEVHAVKP 12
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 IAGTPEVHAVKP 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
                                                                             CIT1.
STATE: MA
COUNTRY: USA
TO 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                         STREET: 60 St
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5-08-433-908B-28
Seguence 28, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                 Sequence 28, Application US/08195947

Sequence 28, Application US/08195947

Patent No. 5840316

GENERAL INFORMATION:

APPLICANT: Smith, Penelope

APPLICANT: Smith, Penelope

APPLICANT: Apidolu, Asil

APPLICANT: Theerakulpisut, Piyada

APPLICANT: Hough, Terryn

APPLICANT: Suphioglu, Cenk

APPLICANT: Suphioglu, Cenk

APPLICANT: Suphioglu, Cenk

TITLE OF INVENTION: Ryegrass Pollen Allergen

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5840316ris

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 48; DB 2; Length 13; Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN ROLEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,947
FILING DATE: 14-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08 07/930,060
FILING DATE: 14-ANG-1992
ATTONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ong, Eng Kok
TITLE OF↓INVENTION: Ryegrass Pollen Allergen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/CDCKET NUMBER: IMPH-0024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR SEO ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
US-08-433-885-28
; Sequence 28, Application US/08433885
; Patent No. 5869333
; GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir
APPLICANT: Singh, Mohan Bir
APPLICANT: Smith, Penelope
APPLICANT: Avjioglu, Asil
APPLICANT: Theerakulpisut, Piyada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hough, Terryn
Suphioglu, Cenk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 16.2
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 IAGTPEVHAVKP 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,908B
FILING DATE: 02-MAY-1995
CLASSIFICATION: 436
SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,885
FILING DATE: 02-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Singh, Mohan Bir
APPLICANT: Knox, Robert B.
APPLICANT: Smith, Penelope
APPLICANT: Avjioglu, Asil
APPLICANT: Thecrakulpisut, Piyada
APPLICANT: Bough, Terryn
APPLICANT: Suphioglu, Cenk
APPLICANT: Ong, Eng Kok
TITLE OF INVENTION: Ryegrass Pollen Allergen
NUMBER OF SUGUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48; DB 2;
Pred. No. 2.4;
0; Mismatches
                                                                                                                                                 NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-039C2D2
TELECOMMUNICATION INFORMATION:
TELEPANE: (617) 227-7400
TELEPAN: (617) 227-7401
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                             Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 20;
                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Griffith, Irwin J.
APPLICANT: Kuo, Mei-chang
APPLICANT: Luqman, Mohammad
TITLE OF INVENTION: T CELL EPITOPES OF RYEGRASS POLLEN
TITLE OF INVENTION: ALLERGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IPC-075 (IMI-040cp)
TELEDOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 4.1;
); Mismatches
                                                                           Score 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48;
                                                                                               Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBP C COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,861
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 60 State Street, suite 510 CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,016
FILING DATE: 31-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                     ; Sequence 15, Application US/08440861
; Patent No. 5710126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-08-440-861-10
Sequence 10, Application US/08440861
Patent No. 5710126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS:
                                                                           16.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,20
                                                                         Query Match 16.2
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 16.2
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide FRAGMENT TYPE: internal
; MOLECULE TYPE: peptide US-08-410-614-28
                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 5:
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Massachusetts
: USA
                                                                                                                                                      44 IAGTPEVHAVKP 55
                                                                                                                                                                          44 IAGTPEVHAVKP 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||| ||||||||
|1 IAGALEVHAVKP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
3Y: linear
                                                                                                                                                                                                                                                RESULT 11
US-08-440-861-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-440-861-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                        ģ
                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6277383ris
!: One Liberty Place - 46th Floor
Philadelphia
                                                                                                                                                                                                                                                                                                           Length 13
                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Singh, Mohan Bir
APPLICANT: Knox, Robert B.
APPLICANT: Smith, Penelope
APPLICANT: Avjioglu, Asil
APPLICANT: Theerakulpisut, Piyada
APPLICANT: Hough, Terryn
APPLICANT: Buphioglu, Cenk
APPLICANT: Ong, Eng Kok
TITLE OF INVENTION: Ryegrass Pollen Allergen
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                       Score 48; DB 2
Pred. No. 2.4;
0; Mismatches
           NAME: Mandragoures, Any E.
RECISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-039C2D4
TELECOMNUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 742-740
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASCIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
PILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 07/930,060
FILING DATE: 14-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: IMPH-0024
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 28, Application US/08410614; Patent No. 6277383; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 28:SEQUENCE CHARACTERISTICS:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                  LENGTH: 13 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                               Query Match 16.2
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 13 amino acids
                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-433-908B-28
                                                                                                                                                                                                                                                                                                                                                                                   44 IAGTPEVHAVKP 55
                                                                                                                                                                                                                                                                                                                                                                                                                        1 IAGALEVHAVKP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-410-614-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                     å
                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

us-09-696-169a-19.closed.rai

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43.5; DB 1; Length 36; Pred. No. 34; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Glasberg, Mark H.
APPLICANT: O'TOOLe, Timothy
TITLE OF INVENTION: METHODS FOR IDENTIFYING INHIBITORS
TITLE OF INVENTION: OF INTEGRIN ACTIVATION
INMERS OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                         APPLICALL...
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFRENCE/COCKET NUMBER: 06410/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street CITY: Boston STATE: Massachusetts COUNTRY: U.S.A.

ZIP: 02110-2804 COMPUTER READABLE FORM: MSDIUM TYPE: 3.5" Diskette, 1.44 Mb MSDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER: IBM PS/2 Model 502 or 553X OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: WordPerfect (Version 5.1) CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/02885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/214,770
FILING DATE: March 14, 1994
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, PAUL T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06410/002001
TELECOMMUNICATION INFORMATION:
   OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordberfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/214,770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SED ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 52.9%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617) 542-8900
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 YNAAYNAAD-HAAPEDK 29
                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US95-02885-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-214-770-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.8%; Score 44; DB 1; Length 20; 72.7%; Pred. No. 14;
GENERAL INFORMATION:
APPLICANT: Griffith, Irwin J.
APPLICANT: Kuo, Mei-Chang
APPLICANT: Luqman, Mohammad
TITLE OF INVENTION: T CELL EPITOPES OF RYEGRASS POLLEN
TITLE OF INVENTION: ALLERGEN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:

APPLICATION NUBBR: US/08/440,861
FILING DATE: 15-MAY-1995
CLASSIFICATION 435
PRICR APPLICATION DATA:

APPLICATION NUBBR: US 08/106,016
FILING DATE: 31-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-540
INFORMATION FOR SEG ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/08214770
Patent No. 5523209
GENERAL INFORMATION
APPLICANT: Ginsberg, Mark H.
APPLICANT: O'Toole, Tim
TITLE OF INVENTION: INHIBITORS OF INTEGRIN
TITLE OF INVENTION: ACTIVATION
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
                                                                                                                                                                                                                                                                 ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 72.7°,
Thes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-440-861-10
                                                                                                                                                                                                                                                                                                                                                  Massachusetts
. USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :||| |:||||
8 AKAPGLIPKLD 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SKAPQLVPKLD 11
                                                                                                                                                                                                                                                                                              STREET: 60 St
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                            STATE: Mass
COUNTRY: US
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-08-214-770-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
```

õ g

Ή,

Search completed: July 11, 2002, 10:56:11 Job time: 214 sec

```
ij
                                                                                                                                                                                      Gaps
                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08440861
; Patent No. 5710126
; GENERAL INFORMATION:
; APPLICANT: Griffith, Irwin J.
APPLICANT: Lugman, Mohammad
; TITLE OF INVENTION: T CELL FPITOPES OF RYEGRASS POLLEN
; TITLE OF INVENTION: ALLERGEN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
                                                                                                                                               DB 5; Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.8%; Score 41; DB 1; Length 20; 44.4%; Pred. No. 35; 6; Indels tive 4; Mismatches 6; Indels
                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Massachuselle
COMPUTR: USA
ZIP 0130
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,861
FILING DATE: 15-MAY-1995
CLASSIFICATION 0473
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,016
FILING DATE: 31-AGG-1993
ATTORNEY/AGENT INFORMATION:
AMME: Amy E. MANGAGOUTAS
REGISTRATION NUMBER: 36,207
RESERENCE/DOCKET NUMBER: 1PC-075 (IMI-040cp)
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEG ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acid
TOPOLOGY: Linear
MOLECULE TYPE: internal
                                                                                                                                             Score 43.5; DE
Pred. No. 34;
3; Mismatches
                                                                                                                                          Query Match
Best Local Similarity 52.9%;
Matches 9; Conservative
                                                                                                                                                                                                                       14 YNAAYNAAD-HAAPEDK 29
                                                                                                                                                                                                                                              Best Local Similarity 44.4
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
STATE: Massachusetts
COUNTRY: USA
LENGTH: 36
TYPE: amino acid
STRANDEDNESS:
                                                              ; TOPOLOGY: linear
PCT-US95-02885-8
                                                                                                                                                                                                                                                                                                                                              US-08-440-861-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                           ద
```

ö

Gaps .; 0

> 23 HAAPEDKYEAFVLHFSEA 40 :| | | | :: | | | | : 1 NAPPADKFKIFEAAFSES 18

δλ g

```
Use of the control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 52.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 HAAPED--KYEAFVLHF 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :|:||| || |:
11 NASPEDWAKYHAAVRHY 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S70651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                  (without alignments)
280.746 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               melA protein - Sal
hypothetical prote
hypothetical prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical prote
hypothetical prote
MHC HLA-DR-beta-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical prote hypothetical prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              osteocalcin - emu
osteocalcin - crab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical prote
hypothetical prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein-serine/thr
protein disulfide-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide YY - short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .eukotriene-A4 hyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single stranded DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         conserved hypothet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cholecystokinin/ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide YG - Ameri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ribosomal protein
osteocalcin - cat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ribosomal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     osteocalcin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                     US-09-696-169A-20
277
1 QLVPKLDEVYNAAYNAADHA.....SBALHIIAGTPEVHAVKPGA
                                                                                                              July 11, 2002, 10:58:28; Search time 18.14 Seconds
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                            283138 seqs, 96089334 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                           - protein search, using sw model
                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YYFIS
S70651
S52358
R3KM72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GECT
S50084
G95302
B41397
A26781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T36238
I38225
A33210
D83811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC2208
E71901
A69871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D69141
A95019
S42852
A83629
T05086
S24142
S02208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A61280
B87570
A82359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137543
R5VF32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEMKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pir1:*
pir2:*
pir3:*
pir4:*
                                                                                                                                                                                                                                                                                                                                                                                                       seq l'ength: 0
seq length: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR_71:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38
39
38
38
37
37
37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 36.5
3 36.5
35.36
35.35
35.35
35.35
35.35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.5
34.5
34.5
34.5
34.5
34.5
34
                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                       Scoring table:
                                                                         OM protein
                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB
Maximum DB
                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
```

nitrate reductase	insulin - sperm wh	insulin - finback	insulin - sei whal	insulin - elephant	insulin - goat	insulin - Arabian	insulin - cat	insulin - North Am	insulin precursor	hypothetical prote	gene GFAP gamma pr	hypothetical prote	insulin - American	hypothetical prote	fucosyltransferase
A47694	INWHP	INWHE	INWHIS	INEL	INGI	INCMA	INCT	JQ0362	A59151	T07326	I52659	AE3111	A61125	A33965	878008
7	7	7	-	٦	7	٦	-	7	7	7	7	7	~	~	7
20	51	51	51	51	21	21	51	21	21	21	43	20	51	38	39
12.3	12.3	12.3	12.3	12.3	12.3	12.3	12.3	12.3	12.3	12.3	11.9	11.9	11.9	11.7	11.7
34	34	34	34	. 34	34	34	34	34	34	34	33	33	33	32.5	32.5

## ALIGNMENTS

```
N'Alternate names: pancreatic hormone; pancreatic polypeptide
C;Species: Myoxocephalus scorpius (shorthorn sculpin, daddy sculpin)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 20-Mar-1998
C;Accession: A60309; B2693
R;Conlon, J.M.; Schmidt, W.E.; Gallwitz, B.; Falkmer, S.; Thim, L.
Regul. : Pept. 16, 261-268, 1986
A;Title: Characterization of an amidated form of pancreatic polypeptide from the dadd A;Reference number: A60309; NUID:87176585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 1-36 <CUT>
A; Residues: 1-36 <CUT>
A; Experimental Source: islet organs (Brockmann bodies)
C; Comment: Peptide YY and pancreatic peptide are identical in this fish but are disti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Accession: A60309
A Molecule type: protein
A Residues: 1-36 CON>
A Residues: 1-36 CON CON CONTRACT CONTRACT CON CONTRACT CON CONTRACT CONT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C:Superfamily: pancreatic hormone
C:Keywords: amidated carboxyl end; hormone; pancreas
F:36/Modified site: amidated carboxyl end (Tyr) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.4%; Score 40; DB 1; Length 36; 52.9%; Pred. No. 2.2e+02; tive 3; Mismatches 3; Indels
peptide YY - shorthorn sculpin
```

1;

Gaps

;

```
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-53 < KURA
A; Residues: 1-53 < KURA
A; Cross-references: GB: AE006469; PIDN: AAK64985.1; PID: g14523412; GSPDB: GN00165
A; Experimental source: strain 1021, megaplasmid pSymA
B; Gallbert, F.: Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.L.; Hyman, R.W.; Jones, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; B.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A; Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meli A; Reference number: A§5262; MUID:21396509; PMID:11481432
  N;Alternate names: BGP; bone Gla protein; gamma-carboxyglutamic acid-containing prote C;Species: Felis silvestris catus (domestic cat) C;Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 06-Sep-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein SMa0625 [imported] - Sinorhizobium meliloti (strain 1021) magapl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N.Alternate names: RNA-binding protein H16 - green monkey (fragments)
N.Alternate names: RNA-binding protein K homolog
C; Species: Cercopithecus aethiops (green monkey, grivet)
C; Date: 23-May-1997 #text_change 19-Feb-1999
C; Accession: 550084
R; Gaillard, C.; Cabannes, E.; Strauss, F.
Nucleic Acids Res. 22, 4183-4186, 1994
A; Title: Identity of the RNA-binding protein K of hnRNP particles with protein H16, A; Reference number: 550084; MUID:95023188
                                                                                C; Accession: A03304
R; Shimmura, H; Kanai, Y; Sanada, K.
B; Shimmura, H; Kanai, Y; Sanada, K.
B; Shimmura, H; Kanai, Y; Sanada, K.
B; Biochem. 96, 405-411, 1984
A; Title: Primary structure of cat osteocalcin.
A; Reference number: A03304; MuID:85054706
A; Accession: A03304
A; Molecule type: protein
A; Residues: 1-49 < SHI>
C; Superfamily: osteocalcin
C; Superfamily: osteocalcin
C; Keywords: bone; calcium binding; carboxyglutamic acid; hydroxyproline
F; 9/Modified site: 4-hydroxyproline (Pro) #status experimental
F; 17, 21, 24/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental
F; 23-29/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: G95302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38; DB 2; Ler
Pred. No. 4.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 13.9%; Score 38.5; DB 1; Best Local Similarity 34.5%; Pred. No. 4.9e+02; Matches 10; Conservative 3; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 ELNPDCDEL-----ADHIGFQDAYRF 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QLVPKLDEVYNAAYNAADHAAPEDKYEAF 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 1-16;17-28;29-41 <GAI>
A;Experimental source: cell line CVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 YNAAYNAADHAAPEDKY 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 YNASVXVPDXXGPEGSY 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
Ciscession: 552358
R.Agryrokastritis, A.; Leversha, M.A.; Ferguson-Smith, M.; Moschonas, M.K. submitted to the EMBL Data Library, March 1993
A.Description: A cosmid clone mapped to human chromosome 11p15 detects a Taq I restricts A.Reference number: 552355
A.Accession: 552358
A.Accession: S52358
A.Status: preliminary
A.Status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tibosomal protein S7-2 - Chlamydomonas reinhardtii chloroplast
C;Species: chloroplast Chlamydomonas reinhardtii
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 22-Jun-1999
C;Accession: S11897
R;Robertson, D.; Boynton, J.E.; Gillham, N.W.
Mol. Gen. Genet. 221, 155-163, 1990
A;Title: Cotranscription of the wild-type chloroplast atpE gene encoding the CF(1)/CF(0)
                                                                                                                                                                                                         .;
?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA-A;Residues: 1-43 <AGR>A;Residues: 1-43 <AGR>A;Cross-references: EMBL:X72882; NID:9667005; PIDN:CAA51394.1; PID:9667006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL: X53977; NID: g11429; PIDN: CAA37927.1; PID: g11430 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                         4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Genome: chloroplast
C;Superfamily: Chlamydomonas chloroplast ribosomal protein S7-2
C;Keywords: chloroplast; protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 LVPKLDEVYNAAYNAADHAAPEDKYEAFVLHFSEALHIIAGTPEVHAVKP 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39; DB 1; Length 52; Pred. No. 4.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21; Indels
                                                                                                                                           Score 40; DB 2; Length 49;
Pred. No. 3.2e+02;
9; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39; DB 2; Length 43;
Pred. No. 3.7e+02;
4; Mismatches 13; Indels
A;Cross-references: EMBL:U43411
C;Superfamily: leukotriene-A4 hydrolase
C;Keywords: alternative splicing; ether hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                                   9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 AAPEDKYEAFVLHFSEALHIIAGTPEVHAV 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43
                                                                                                                                                                                                                                                                                            3 VPKLDEVYNAAYNAADHAAPEDKYEAFVLH 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: $11897; MUID:90318312
A; Accession: $11897
A; Molecule type: DNA
A; Residues: 1-52 <ROB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.1%;
30.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.1%;
36.7%;
                                                                                                                                           Query Match 14.4%;
Best Local Similarity 33.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ift mutations in atpE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          osteocalcin -, gat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                            õ
```

Science 293,

ð QΩ

```
Rioliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, March 1999
A; Reference number: 221577
A; Accession: T36238
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-42 < OLID
A; Cross-references: EMBL:AL049573; PIDN:CAB40336.1; GSPDB:GN00070; SCOEDB:SCE39.28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Sapecies: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 05-Nov-1999
C;Accession: I38225; S37427
R;Schultz, S.J; Nigg, E.A.
Cell Growth Differ. 4, 821-830, 1993
A;Tile: Identification of 21 novel human protein Kinases, including 3 members of A;Reference number: I38211; MUID:94100173
A;Reference number: I382125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein disulfide-isomerase (EC 5.3.4.1), pancreatic - dog (fragment)
NyAlternate names: S-S rearrangase
C;Species: Canis lupus familiaris (dog)
C;Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 12-Apr-1995
C;Accession: A33210
R;Michalak, M.
Submitted to the Protein Sequence Database, July 1991
A;Reference number: A33210
A;Accession: A33210
                                   hypothetical protein SCE39.28 - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T36238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL: Z25435; NID: 9405748; PIDN: CAA80922.1; PID: 9405749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 1-27 <MIC>
C;Superfamily: protein disulfide-isomerase; thioredoxin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 2; Length 46;
Pred. No. 7.1e+02;
2; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36.5; DB 2;
Pred. No. 4.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 2; 1
Pred. No. 6.4e+02;
1; Mismatches 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Keywords: intramolecular oxidoreductase; isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein-serine/threonine kinase - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 FGSASHVADNDITPYLVSRFYRAPEIIIG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 YNAADHAAPEDKYEAFVLHFSEALHIIAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: strain A3(2) C; Genetics: A; Gene: SCOEDB: SCE39.28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.4%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.2%;
45.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 13.4%;
Best Local Similarity 34.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 GVPSRHAVREGA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42 GTPEVHAVKPGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-46 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
84.1397
84.1397
84.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.1397
85.13
Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, Hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A;Reference number: A96039; MUID:21368234; PMID:11474104

C;Genetics: annotation

C;Genetics: A;Genetics

A;Gene: SMa0625

A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
A26781
A26781
peptide YG - American goosefish
C;Species: Lophius americanus (American goosefish)
C;Species: Lophius americanus (American goosefish)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 12-Apr-1995
C;Cocession: A26781
R;Andrews, P.C.; Hawke, D.; Shively, J.E.; Dixon, J.E.
Endocrinology 116, 2677-2681, 1985
A;Title: A nonamidated peptide homologous to porcine peptide YY and neuropeptide YY.
A;Reference number: A26781; MUID:85203740
A;Reference number: A26781
A;Residues: 1-37 cAND>
C;Superfamily: pancreatic hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5,
                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 2; Length 53;
Pred. No. 6.2e+02;
2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37; DB 2; I
Pred. No. 5.5e+02;
4; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 2
Pred. No. 5e+02
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A41397; MUID:90190650
A; Accession: B41397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                         13.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.48;
                                                                                                                                                                                                                                                                                                                                                                                  Query Match 13.7°
Best Local Similarity 41.2
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 AFVLHFSEALHIIAGTP 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 AFMLFLOSVVHAFAGOP 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAAPED--KYEAFVLHF 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|:||| |:| |: | |: | NASPEDWASYQAAVRHY 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: mRNA
Residues: 1-34 <MILS
A;Cross-references: GB:M32745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 HFSEALHIIAGTPEVH 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : | : | : |: | | | YFVQGLPALPGSPEAH 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 6; Conserv
```

Query Match

g ö

19

õ g RESULT

a f

ö

ö

;;

Gaps

4

Score 36; DB 2; Leuy...... Pred. No. 9.9e+02;

3; Mismatches

```
C; Accession: E71901
R; Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D. i. Ilos, C. Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F. Nature 397, 176-180, 1999
A; Title: Genomic sequence comparison of two unrelated isolates of the human gastric p. A; Reference number: A71800; MUID:99120557
A; Accession: E71901
A; Accession: E71901
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-48 cARN>
A; Residues: 1-48 cARN>
A; Residues: 1-48 cARN>
A; Cross-references: GB: AE001500; GB: AE001439; NID: 94155238; PIDN: AAD06268.1; PID: 9415
C; Genetics: A; Gene: jhp0693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 DEVYNAAYNAADHAAPEDKYEAFVLHFSE 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 DEEYNDYKNVYD----DDDYEDYNSDYEE 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: July 11, 2002, 11:00:38
Job time: 130 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 13.0%;
Best Local Similarity 34.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein asr3218 [imported] - Anabaena sp. (strain PCC 7120)
C;Species: Anabaena sp.
A;Notee Anabaena sp.
A;Notee Anabaena sp.
C;Species: Anabaena sp.
C;Species: Anabaena sp.
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C;Accession: AC2208
R;Kan&co, T., NaKamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Residues: 1-52 cKUR>
A;Rolecule type: DNA
A;Residues: 1-52 cKUR>
A;Cross-references: GB:BA000019; PIDN:BAB74917.1; PID:g17132313; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: asr3218
                                                                                                                                                                                                                                                           C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Dates: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Datesion: B83811
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Accession: D83811
A;Accession: D83811
A;Accession: D83811
A;Residues: 1-39 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BAB05011.1; GSPDB:GN00 A;Experimental source: strain C-125 C;Genetics: A;Gene: BH1292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein jhp0693 - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
                                                                                                                                                                                                                             hypothetical protein BH1292 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
        Gaps
        3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .,
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
        Indels
        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36.5; DB 2;
Pred. No. 6.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36.5; DB 2;
Pred. No. 9.4e+02;
5; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Mismatches
        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 KLDEVYNAAY -- NAA -- - DHAAPEDKYEAFV 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 KANDLYKNEFISNGAEWNDFIAQEAKYQSFI 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 EAFVLH-----FSEALHIIAGTPEV 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               э;
е
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.2%;
32.3%;
                                                                                           2 APDEEDHVLVLHKGNFDEAL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.2%;
ilarity 32.0%;
Conservative
                                                            21 APEDKYEAFVLH---FSEAL 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Conservative
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity
' has 8; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 10; Conserva
     .
ن
     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                            à
                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
```

ĕ

```
MEDLINE-87176585; PubMed-3562898;

MEDLINE-87176585; PubMed-3562898;

Conlon J.M., Schmidt W.E., Gallwitz B., Falkmer S., Thim L.;

Conlon J.M., Schmidt W.E., Gallwitz B., Falkmer S., Thim L.;

"Characterization of an amidated form of pancreatic polypeptide from the daddy sculpin (Cottus scorpius).";

Regul. Pept. 16:261-2681989;

C: -: SUBCELLULAR LOCATION: Secreted.

C: -: SIMILARITY: BELONGS TO THE NPY / PPY / PYY FAMILY.

RP PIR, A60309; YYFIS.

R HSSP; PO1303; 1RON.

R InterPro; IPR001955; Pancreatic_hormn.

R PRODOM; PR001267; Pancreatic_hormn; 1.

R PRODOM; PR001267; PANCREATIC_HORMONE_1; 1.

R PROSITE: PS50276; PANCREATIC_HORMONE_2; 1.

M HORTOME: Amidation.
                                                                                                                               bovine coro
ectothiorho
                                                                                 bacteriopha
  axinella po
                          lepisosteus
                                            rana ridibu
                                                                  canis famil
                                                                                                           mus musculu
                                                                                                                                                                         vipera lebe
                                                                                                                                                                                               rana escule
                                                                                                                                                                                                                 oncorhynchu
                                                                                                                                                                                                                                     arthrobacte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myoxocephalus Scorpius (Shorthorn sculpin) (Daddy sculpin).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
Cottoidei; Cottidae; Myoxocephalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-87190954; PubMed-2883025;
Cutfield S.M., Carne A., Cutfield J.F.;
"The amino-acid sequences of sculpin islet somatostatin-28 and
peptide YY.";
FEBS Lett. 214:57-61(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3
                                       P29204
P92204
P32284
P09542
P15778
P80105
P81375
P40837
P09474
  P28588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMIDATION.
16F331B73643D7AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 1;
Pred. No. 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                            36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                 REPA_BPT4
MLEV_MOUSE
VNS1_CVBM
                                                                                                                                                                       OXLA_VIPLE
BR2A_RANES
PYY_ONCKI
                                         PYY_RANRI
APAF_CANFA
                                                                                                                                                 LHB2_ECTHA
                                                                                                                                                                                                                                       RL7_ARTGL
                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.4%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA; 4170 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 HAAPED -- KYEAFVLHF 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|:||| || || |:
11 NASPEDWAKYHAAVRHY 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
  Peptide YY-like (PYY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 9; Conserv
111.2
111.2
111.2
111.2
111.0
111.0
111.0
111.0
111.0
111.0
111.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36
                                                                                                                                                                                                                                                                                                                                                                                                            PYY_MYOSC
P09641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOD_RES
SEQUENCE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                    PYY_MYOSC
AC DE POYALM
DT 01-MA DT 02-MA DT 02-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
PYY_RAJRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
334
337
44
44
54
54
54
54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                     (without alignments)
201.982 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hystrix cri
ornithorhyn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oreochromis
felis silve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      elephas max
felis silve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rattus norv
katsuwonus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dromaius no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   xenopus lae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       synechococc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               balaenopter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  didelphis m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anguilla ro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acomys cahi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       trachemys s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acipenser g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lepisosteus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carassius a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            myoxocephal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         macaca fasc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  balaenopter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            capra hircu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anser anser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               devario pat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   puntius tet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               canis famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           danio kerri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  raja rhina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vicia faba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        camelus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                          QLVPKLDEVYNAAYNAADHA.....SEALHIIAGTPEVHAVKPGA
                                                                                                                                            July 11, 2002, 11:00:43; Search time 10:16 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P02821
P81555
P02819
P02819
P02819
P02819
P01314
P01312
P01324
P01328
P0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          013253
P79855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P29206
P81028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P79715
                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                         hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                    105224 seqs, 38719550 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYY_MYOSC
PYY_RAJRH
PYY_ORENI
OSTC_FELCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OSTC_CANFA
OSTC_DRONO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OSTC_RABIT
OSTC_RABIT
OSTC_XENLA
PSBK_STNEL
RK3.2_VICFA
INS_BALBO
INS_BALBO
INS_BALPH
INS_CAPHI
INS_CAPHI
INS_CAPHI
INS_CAPHI
INS_ELEMA

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TWHH_DEVPA TWHH_PUNTE
                                                                                                       protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OSTC_MACFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INS_TRASC
INS_ACIGU
INS_LEPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WHH_CARAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WHH_DANKE
                                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                       US-09-696-169A-20
277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SwissProt_40:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0 Maximum DB seq length: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                                                                Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.5
33
32.5
32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                            Sedneuce:
                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š.
```

;;

ij

Gaps

```
PIR, A03304; GECT.
InterPro: IPR0002384; GLA_bone.
InterPro: IPR000294; VitK_dep_GLA.
Pfam: PF00594; gla; 1.
PRINTS: PR00002; GLABONE.
SMART: SM00069; GLA:
PROSTTE: PS00001; GLU_CARBOXXLATION; 1.
Calcium-binding; Gamma-carboxyglutamic acid; Vitamin K; Hydroxylation;
                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Osteocalcin (Gamma-carboxyglutamic acid-containing protein) (Bone Glaprotein) (BGP).
                                                                                                                                                                                                                                                                                                                                                                                    Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
NCBI_TaxID=9685;
                                                                                    5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.9%; Score 38.5; DB 1; Length 49; 34.5%; Pred. No. 1.7e+02;
                                                           Score 39; DB 1; Length 36;
Pred. No. 1.1e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
             AMIDATION (BY SIMILARITY). 0246CFBC6243D7AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93D2131FA9F656D3 CRC64;
                                                                                                                                                                                           49 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYDROXYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QLVPKLDEVYNAAYNAADHAAPEDKYEAF 29
                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-85054706; Pubmed-6334077;
Shimomura H., Kanai Y., Sanada K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21
24
29
5495 MW;
                                                            14.1%;
56.2%;
             36 36
36 AA; 4201 MW;
                                                           Query Match 14.1
Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                            20 AAPED -- KYEAFVLHF 33
                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
 Hormone; Amidation.
MOD_RES 36
SEQUENCE 36 AA; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 AA;
                                                                                                                                                                                           OSTC_FELCA
P02821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OSTC_CANFA P81455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD_RES
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
OSTC_CANFA
                                                                                                                                                                                 OSTC_FELCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bone
   SO ET
                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PT PT
                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95384941; PubMed-7656183;

Nguyen T.M., Wright J.R. Jr., Nielsen P.F., Conlon J.M.;

"Characterization of the pancreatic hormones from the Brockmann body of the tilapia: implications for islet xenograft studies.";

Comp. Biochem. Physiol. 111C:33-44(1995).

-! SUBCELLULAR LOCATION: Secreted.
-! SIMILARITY: BELONGS TO THE NPY / PPY / PYY FAMILY.

HSSP; P01303; 1RON.

InterPro; IPR001955; Pancreatic_hormn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
Cichlidae; Oreochromis.
                                                                    Raja rhina (Skate).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
Rajiformes; Rajidae; Raja.
                                                                                                                                                     2;
                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB 1; Length 36;
Pred. No. 79;
                                                                                                                                                                                                                                                                                                                                                                                                                          6; Indels
                                                                                                                                                                                                                                                                                                                                                  AMIDATION.
07A7D9DC196660B6 CRC64;
                       01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Peptide YY-like (PYY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Peptide YY-like (PYY).
 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS, PRO0278; PANCHORMONE.
Prodbm; PD001267; Pancreatic_hormn; 1.
SMART; SM03109; PAH; 1.
PROSITE; PS00265; PANCREATIC_HORMONE_1; 1.
PROSITE; PS50276; PANCREATIC_HORMONE_2; 1.
                                                                                                                                                                                                                                                                       PRINTS: PRO0278; PANCHORMONE.
ProDom: PD001267; Pancreatic_hormn; 1.
PROSTIE; PS00265; PANCREATIC_HORMONE_1;
PROSTIE; PS50276; PANCREATIC_HORMONE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 NAADHAAPED -- KYEAFVLHF 33
                                                                                                                                                                                                                                                                                                                                                                                                  14.48;
                                                                                                                                                                                                                                                                                                                                                  36 36
36 AA; 4251 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                          9; Conservative
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                     Hormone; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                      NCBI_TaxID=30478;
PYY_RAJRH
P29206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYY_ORENI
P81028;
                                                                                                                                                                                                                                                                                                                                                  MOD_RES
SEQUENCE
                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PYY_ORENI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

1;

Gaps

```
SIMILARITY: BELONGS TO THE OSTEOCALCIN / MATRIX GLA-PROTEIN
                                                                                                                                                                                                                                                                                  Score 34.5; DB 1;
Pred. No. 5.5e+02;
4; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                             1 QLVPKLDEVYNAAYNAADHAAPEDKYEAF 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002384; GLA_bone.
InterPro; IPR000294; VitK_dep_GLA.
Pfam; PF00594; gla; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-82182842; PubMed-6978733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
17
21
24
29
5743 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.5%;
                                                                                                                                                                                                                                                                                                                 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00002; GLABONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A03302; GEMKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein) (BGP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  OSTC_MACFA P02819;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOD_RES
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOD_RES
MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
OSTC_MACFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BGLAP
                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00539; 913; 1.
PRIMIS; PR00002; GLABONE.
SMART; SM00069; GLA: 1.
PROSITE; PS00011; GLU_CARBOXXLATION; 1.
Calcium-binding; Gamma-carboxyglutamic acid; Vitamin K; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Osteocalcin (Gamma-carboxyglutamic acid-containing protein) (Bone Gla-
    01-MRR-2002 (Rel. 41, Last annotation update)
Osteocalcin (Gamma-carboxyglutamic acid-containing protein) (Bone Gla-
                                                                                                                                                                                                                 J. Bone Miner. Res. 8:733-743(1993).
-!- FUNCTION: CONSTITUTES 1-2% OF THE TOTAL BONE PROTEIN. IT BINDS STRONGLY TO APATITE AND CALCIUM.
-!- PTM: GAMMA-CARBOXYGIATION. THESE RESIDUES ARE FORMED BY VITAMIN K
DEPENDENT CARBOXYLATION. THESE RESIDUES ARE ESSENTIAL FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hud N.L., Tseng A., Chapman G.E.;
"The amino acid sequence of Emu osteocalcin: gas phase sequencing of Gla-containing proteins.";
Blochem. Int. 15:271-277(1987).
-!- FUNCTION: CONSTITUTES 1-2% OF THE TOTAL BONE PROTEIN. IT BINDS STRONGLY TO APASTITE AND CALCIUM.
-!- FUNCTION: CARBOXYGILATION THESE RESIDUES ARE FORMED BY VITAMIN K DEPENDENT CARBOXYGILATION. THESE RESIDUES ARE ESSENTIAL FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Palaeognathae; Casuariiformes; Dromaiidae;
                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE OSTEOCALCIN / MATRIX GLA-PROTEIN FAMILY.
                                                                                                                                                                        Colombo G., Fanti P., Yao C., Malluche H.H.; "Isolation and complete amino acid sequence of osteocalcin from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYDROXYLATION (BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 37.5; DB 1; Length 49;
Pred. No. 2.3e+02;
5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43121D015817CEA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QLVPKLDEVYNAAYNAADHAAPEDKYEAF 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002384; GLA_bone.
InterPro; IPR000294; VitK_dep_GLA.
                                                                                                                                                          MEDLINE=93318657; PubMed=8101026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-88134266; PubMed=3501719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dromaius novae-hollandiae (Emu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.5%;
31.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
17
21
24
29
5524 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                 BINDING OF CALCIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity
Matches 9; Conserv
                                                                                                            NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein) (BGP).
                                    protein) (BGP).
                                                                                                                                                                                                        canine bone."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OSTC_DRONO
P15504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOD_RES
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C_DRONO
```

ij

Gaps

7;

9; Indels

```
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
0steocalcin (Gamma-carboxyglutamic acid-containing protein) (Bone Gla-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00069; GLA; 1. PROSITE; PS00011; GLU_CARBOXYLATION; 1. Calcium-binding; Gamma-carboxyglutamic acid; Vitamin K; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hauschka P.V., Carr S.A., Biemann K.;
"Primary structure of monkey osteocalcin.";
Blochemistry 21:638-642(1982).
-!- FUNCTION: CONSTITUTES 1-2% OF THE TOTAL BONE PROTEIN. IT BINDS STRONGLY TO APATITE AND CALCIUM.
-!- PTM: GAMMA-CARBOXYGLUTAMIC ACID RESIDUES ARE FORMED BY VITAMIN DEPENDENT CARBOXYLATION. THESE RESIDUES ARE ESSENTIAL FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BINDING OF CALCIUM.
-!- SIMILARITY: BELONGS TO THE OSTEOCALCIN / MATRIX GLA-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
C20116014D0C4958 CRC64;
                                                                                                                                                                            49 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYDROXYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34.5;
23 ELNPDCDEL-----ADHIGFQEAYRF 44
```

```
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=32046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSBK_SYNEL
                  Amphibia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09F1K9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSBK_SYNEL
                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDT TDD DDT DD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002384; GLA_bone.
InterPro; IPR00294; VitK_dep_GLA.
Pfam; PF00594; gla; 1.
PRINTS; PR00002; GLABONE.
SMART; SM00069; GLA; 1.
PROSITE; PS00011; GLU_CARBOXXLATION; 1.
Calclum-binding; Gamma-carboxyglutamic acid; Vitamin K; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-07T-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Osteocalcin (Gamma-carboxyglutamic acid-containing protein) (Bone Gla-
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-92175242; pubmed-1794506;
Virdi A.S., Willis A.C., Hauschka P.V., Triffitt J.T.;
Virdi A.S., Willis A.C., Hauschka P.V., Triffitt J.T.;
Primary aminoacid sequence of rabbit osteocalcin.";
Blochem. Soc. Trans. 19:1338-3738(1991).
-!- FUNCTION: CONSTITUTES 1.2% OF THE TOTAL BONE PROTEIN. IT BINDS STRONGLY TO APATITE AND CALCIUM.
-!- PTW. GAMMA-CARBOXYGLOTAMIC ACID RESIDUES ARE FORMED BY VITAMIN DEPENDENT CARBOXYLATION. THESE RESIDUES ARE ESSENTIAL FOR THE
                                                                                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein) (BGP).
Xenopus laevis (African clawed frog).
Eukaryots, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE OSTEOCALCIN / MATRIX GLA-PROTEIN
                                                                                                                                                                                                                                                                              (Rel. 31, Last sequence update)
(Rel. 41, Last annotation update)
(Gamma-carboxyglutamic acid-containing protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYRROLIDONE CARBOXYLIC ACID
                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYDROXYLATION.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
7B218871F0312253 CRC64;
. 5.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34.5; DB 1;
Pred. No. 5.6e+02;
4; Mismatches 9;
                                                                                                                                                                                                                      49 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 5.664; Mismatches
                Pred. No. 5.66
; Mismatches
                                                                          29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 ELNPDCDEL-----ADHIGFQEAYRF 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QLVPKLDEVYNAAYNAADHAAPEDKYEAF 29
                                                                          1 QLVPKLDEVYNAAYNAADHAAPEDKYEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                           (Rel. 31, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.5%;
31.0%;
                Best Local Similarity 31.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5431 MW;
                                                                                                                                                                                                                                                                                                                                          (Bone Gla-protein) (BGP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BINDING OF CALCIUM
                                                                                                                                                                                                                                                                              01-FEB-1995 (Rel. 31, 01-MAR-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A61280; A61280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9986;
                                                                                                                                                                                                                                                         01-FEB-1995
                                                                                                                                                                                                                                                                                                                     Osteocalcin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OSTC_XENLA
P40147;
                                                                                                                                                                                                                    OSTC_RABIT
P39056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOD_RES
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD_RES
MOD_RES
MOD_RES
MOD_RES
                                                                                                                                                                              RESULT 8
OSTC_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OSTC_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                            ŏ
                                                                                                                g
                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OS DE DI DI SCO
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                   Cancela M., Williamson M.K., Price P.A.; "Amino-acid sequence of bone Gla protein from the African clawed toad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                   Xenopus laevis and the fish Sparus aurata.";
Int. J. Pept. Protein Res. 46:419-423(1995).
-!- FUNCTION: CONSTITUTES 1-2% OF THE TOTAL BONE PROTEIN. IT BINDS STRONGLY TO APATITE AND CALCIUM.
-!- PTM: GAMMA-CARBOXYCLATION: THESE RESIDUES ARE ESSENTIAL FOR THE DEPENDENT CARBOXYLATION. THESE RESIDUES ARE ESSENTIAL FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Katoh H., Ikeuchi M.; "Cloning and disruption of the psbK gene from thermophilic Thermosynechococcus elongatus."; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-:- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE REACTION CENTER OF PHOTOSYSTEM II.
                                                                                                                                                                                                                                                                                                                                                                                                           -1- SIMILARITY: BELONGS TO THE OSTEOCALCIN / MATRIX GLA-PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Photosystem II reaction center protein K precursor (PSII-K).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synechococcus elongatus (Thermosynechococcus elongatus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cyanobacteria; Chroococcales; Synechococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34.5; DB 1;
Pred. No. 5.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE PSBK FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QLVPKLDEVYNAAYNAADHAAPEDKYEAF 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                   MEDLINE=96139691; PubMed=8567186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB052850; BAB20628.1; -. InterPro; IPR003687; PsbK. Pfam; PF02533; PsbK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.5%;
31.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 12.5
Best Local Similarity 31.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                         BINDING OF CALCIUM
                            Xenopodinae; Xenopus.
NCBI_TaxID=8355;
```

```
21-JUL-1986
21-JUL-1986
01-OCT-1996
                           INS_BALBO
P01314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INS_BALPH
P01312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_CONS
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                  SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insulin.
                                                                                            Insulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
              INS_BALBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INS_BALPH
                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
            BY SIMILARITY.
PHOTOSYSTEM II REACTION CENTER PROTEIN K.
45C5197F4B50E398 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=90206803; PubMed=2320425;
Herdenberger F., Pillay D.T.N., Steinmetz A.;
Herdenberger F. Pillay D.T.N., Steinmetz A.;
Sequence of the trnH gene and the inverted repeat structure deletion
site of the broad bean chloroplast genome.";
Nucleic Acids Res. 18:1297-1297(1990).
                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Vicia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=89208884; PubMed=3242868;
Herdenberger F., Weil J.H., Steinmetz A.;
Herdenberger F., Weil J.H., Steinmetz A.;
"Organization and nucleotide sequence of the broad bean chloroplast
genes trn-UAG, ndhF and two unidentified open reading frames.";
Curr. Genet. 14:609-615(1988).
-!- SIMILARITY: BELONGS TO THE L32P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.3%; Score 34; DB 1; Length 48; 42.9%; Pred. No. 6.4e+02;
                                                                          Score 34; DB 1; Length 46; Pred. No. 6.1e+02; 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribosomal protein; Chloroplast.
SEQUENCE 48 AA; 5407 MW; 146372D6C9BC34DB CRC64;
                                                                                                                                                                                                                                                 01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-FBB-1996 (Rel. 33, Last annotation update)
Chloroplast 50s ribosomal protein L32.
                                                                                                                                                                                                                         48 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S08495; R5VF32.
PIR; S08444; S08444.
Mendel, 5435; VICEA: rpl32;1.
InterPro; IPR002677; Ribosomal_L32p.
Pfam; PF01783; Ribosomal_L32p.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 YEAFVLHFSEALHIIAGTPEV 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 YKAALKAFSLADSILTGTSKV 45
                                                                          12.3%;
40.0%;
            9
46
5026 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X51471; CAA35833.1; -.
                                                                                         Best Local Similarity 40.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                 Vicia faba (Broad bean).
                                                                                                                              35 EALHIIAGTPEVHAV 49
                                                                                                                                              : | | :: | | | :|: | 3 DALVLVAKLPEAYAI 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                      46 AA;
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3906;
Photosystem II.
                                                                                                                                                                                                                                                01-APR-1990 (
01-APR-1990 (
01-FEB-1996 (
                                                                                                                                                                                                                                                                                                                             Chloroplast.
                                                                                                                                                                                                                         RK32_VICFA
P15820;
                                       SEQUENCE
                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
            PROPEP
                                                                                                                                                                                               RESULT 11
RK32_VICFA
FT
                                                                                                                               ð
                                                                                                                                                      g
                                                                                                                                                                                                                       ò
```

```
ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                             -1- FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. IT INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS AND FATTY ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE CYCLES, AND GLYCOGEN SYMTHESIS IN LIVER.
                                                                                                                                                                                                                                                                                              Ishihara Y., Saito T., Ito Y., Fujino M.;
Structure of sperm- and sei-whale insulins and their breakdown by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Physeter catodon (Sperm whale) (Physeter macrocephalus).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Cetacea, Mysticeti,
                                                                                                                                            Balaenoptera borealis (Sei whale).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ٠.
ف
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Balaenoptera physalus (Finback whale) (Common rorqual), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFIDE BONDS.

-: SUBCELDULAR LOCATION: Secreted.

-:- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

PIR; A01582; INWH1S.

FRSP; PO1115; 91NS.

InterPro; IPRO00739; Insulin_IGF_relaxin.

PF00049; Insulin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34; DB 1; Length 51;
Pred. No. 6.8e+02;
5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9007B50E400A7DDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                   (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INSULIN B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INSULIN A CHAIN.
Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insulin family; Hormone; Glucose metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 HFSEALHIIAG-----TPEVHAVK 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Balaenopteridae; Balaenoptera.
NCBI_TaxID=9768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Balaenopteridae; Balaenoptera.
NCBI_TaxID=9770, 9755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.3%;
32.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5723 MW;
                                                                                                                                                                                                                                                                                                                                        whale pepsin.";
Nature 181:1468-1469(1958)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00276; INSULINA. PRINTS; PR00277; INSULINB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 32.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00078; IIGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES=B.physalus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PARTIAL SEQUENCE
```

```
FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE
                                                                                                                  PIR; A92782; INCMA.
HSSP: P01317; ZINS.
InterPror; IFRO00739; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin; 1.
PRINTS; PR00276; INSULINA.
PRINTS; PR00277; INSULINA.
SMART; SM00078; ILGF; 1.
PR0STE; PS00262; INSULIN.
Insulin family; Hormone; Glucose metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INSULIN B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INSULIN A CHAIN.
                                                                                                                                                                                                                                                                                                 INSULIN B CHAIN.
                                                                                                                                                                                                                                                                                                                                        INSULIN A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insulin family; Hormone; Glucose metabolism.
CHAIN 1 30 INSULIN B CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A01586; INGT.
HSSP; P01315; 91NS.
InterPro; IPR000739; Insulin_IGF_relaxin.
                                                                                                                                                                                                                                                                                                                                                             INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                               INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | |||::: | ||:
10 HLVEALYLVCGERGFFYTPKAGIVE 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 HFSEALHIIAG-----TPEVHAVK 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=66160119; PubMed=5949593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEGM: PF00049; INSULIN: 1.
PRINTS; PR00276; INSULINA.
PRINTS; PR00277; INSULINB.
SMART: SM00078; ILGF: 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.3%;
32.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                    5693 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    51 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith L.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INS_CAPHI
P01319;
                                                                                                                                                                                                                                                                                                                  NON_CONS
CHAIN
                                                                                                                                                                                                                                                                                                                                                                           DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_CONS
CHAIN
                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [nsulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
INS_CAPHI
                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                  PRECIES-P. catodon;

Harris J.I., Sanger F., Naughton M.A.;

"Species differences in insulin.";

"Species differences in insulin.";

"Inches Insulin.";

-I- FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. IT

INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS AND
FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE

CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.

-I- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dromfedarius).";
J. Fac. Med. Baghdad 14:16-28(1972).
-!- FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. IT
INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS AND
                                                                                     SPECIES-P.catodon;
Ishihara Y., Saito T., Ito Y., Fujino M.;
"Structure of sperm- and sei-whale insulins and their breakdown by whale pepsin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Camelus dromedarius (Dromedary) (Arabian camel).
Eukaryota Metazoa, Chordatu, Craniata, Vertebratu, Euteleostomi,
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
NCBL_TaxID=9838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Danho W.O.; "The isolation and characterization of insulin of camel (Camelus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
PIR; A91918; INWHF.
PIR; A93142; INWHP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9007B514691A7CDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB 1; Ler
Pred. No. 6.8e+02;
Hama H., Titani K., Sakaki S., Narita K.;
"The amino acid sequence in fin-whale insulin.";
J. Biochem. 56:285-293(1964).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INSULIN A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INSULIN B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insulin family; Hormone; Glucose metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP, P01315; 91NS.
InterPro; IPR000739; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin_1.
PRINTS; PR00276; INSULINA.
PRINTS; PR00277; INSULINB.
SMART; SM00078; IIGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 HFSEALHIIAG-----TPEVHAVK 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 HLVEALYLVCGERGFFYTPKAGIVE 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 01, Created)
(Rel. 01, Last sequ
(Rel. 33, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5766 MW;
                                                                                                                                                                           Nature 181:1468-1469(1958).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (
21-JUL-1986 (
01-FEB-1996 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INS_CAMDR
P01320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                 SEQUENCE.
                                                                                                                                                                                                                        SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_CONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INS CAMDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RREAR REAR RREAR R
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Species variation in the amino acid sequence of insulin.";
Am. J. Med. 40:662-666(1966)
-!- D. Med. 40:662-666(1966)
-!- EUNCTION: INSULIN BECREASES BLOOD GLUCOSE CONCENTRATION. IT
INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS AND
FRATY ACIDS. IT ACCELERATES GITCOLYSIS, THE PENTOSE PHOSPHATE
CYCLE, AND GLYCOGEN SYMTHESIS IN LIVER.
-!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                          TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Capra hircus (Goat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Capra.
                                          BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
9
CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.
SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED
DISULFIDE BONDS.
                                                                                                               -i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB 1; Length 51;
Pred. No. 6.8e+02;
5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   901E88BA085A7DDD CRC64;
```

1;

```
1;
                                                                                     6; Gaps
                                                             Ouery Match
Best Local Similarity 32.0%; Pred. No. 6.8e+02;
Matches 8; Conservative 5; Mismatches 6; Indels
 37 INTERCHAIN.
41 5692 MW; 9007BSOCDB4E7DDD CRC64;
                                                                                                     32 HFSEALHIIAG-----TPEVHAVK 50
 7
19
36
51 AA;
DISULFID
DISULFID
DISULFID
SEQUENCE
 FF
```

Search completed: July 11, 2002, 11:04:00 Job time: 197 sec

δy

Op

ĕ

```
034405 bacillus su
09kg4 clostridium
03427 yersinia pe
0931h2 sulfitobact
09691 homo sapien
026422 methanother
09n1z2 leishmania
                                                                                                                                                                                                      052116 procella ab
052635 brucella me
095ny7 drosophila
094nr2 drosophila
092nw6 enterococcu
09a5y4 caulobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                                                                                                                               Ogfeyl heterocapsa
Ogkvk5 vibrio chol
Ogi814 drosophila
                                                                                                                                                        _097sz7 streptococc
Q9t1j8 bacteriopha
                                                                                                                                                                               049699 arabidopsis
Q91627 pseudomonas
                                                O56128 porcine cir
O91861 porcine cir
                                                                                                                                                                                                                                                                             Qgmhl macaca mula
Q95mk3 ateles belz
Q9nlz1 leishmania
                        Q939r3 bacillus th
Q9r656 rhodobacter
 Q45678 bacillus su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Viriáiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I; Fabales, Fabaceae, Papilionoideae, Phaseoleae, Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pattern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
&
           09z187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN—CV. CLARK;
MEDLINE=20044090; PubMed=10579489;
Stromvik M.V., Sundararaman V.P., Vodkin L.O.;
"A novel promoter that is active in a complex developmental with and without its proximal 650 base pairs.";
Plant Mol. Biol. 41:217-231(1999).
EMBL; AJ293440; CAB96562.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 AA; 4935 MW; 2327B258B8A2CFA5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44; DB 10; L
Pred. No. 1.6e+02;
6; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 YNAADHAAPE-DKYEAFVLHFSEALHIIAGTPEVHAVK 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 AA
                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAJOR LATEX PROTEIN HOMOLOGUE (FRAGMENT).
Q45678
Q92L87
Q939R3
Q9R656
O56128
O91861
                                                                                                        093LH2
096EJ1
026422
09NLZ2
097SZ7
                                                                                                                                                                                                                                        09W1R2
09ZHW6
09A574
                                                                                                                                                                                         Q91627
O52116
O52635
Q95NY7
                                                                                                                                                                                 049699
                                                                                 09KGZ4
034277
                                                                                                                                                                                                                                                                                                                 Q9FEY1
                                                                                                                                                                                                                                                                                                                              Q9KVK5
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                               Q9GMH1
                                                                                                                                                                                                                                                                                          095MK3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.9%;
31.6%;
                        Local Similarity 31.6 nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                   Glycine max (Soybean)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CV. CLARK;
Vodkin L.O.;
 NCBI_TaxID-3847
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000
01-OCT-2000
01-MAR-2001
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9LEJS
Q9LEJS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
Q9LEJ5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best
 Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09163 glycine max 018822 sus scrofa 0204td6 sus scrofa 0202801 streptomyce 027271 plasmodium m 09281 rhizobium m 09281 streptomyce 025213 plasmodium 026213 plasmodium 026213 plasmodium 026213 plasmodium 0984c1 bacillus ha
                                                                                            (without alignments)
382.668 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q91ej5 glycine max
Q91e39 glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ogapq5 uncultured
Ogrid3 yersinia pe
Ogvq65 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              number of results predicted by chance to have a an or equal to the score of the result being printed, y analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                     QLVPKLDEVYNAAYNAADHA.....SEALHIIAGTPEVHAVKPGA
                                                                               July 11, 2002, 11:00:18 ; Search time 23.96 Seconds
                                                                                                                                                                                                                                           33061
           4.5
Compugen Ltd.
                                                                                                                                                                                                                                       hits satisfying chosen parameters:
                                                                                                                                                                                                                  562222 seqs, 172994929 residues
           GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                          - protein search, using sw model
                                                                                                                                                                                                                                                                                                                           Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9RID3
Q9VQ65
Q9LEJ3
                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9LEJ5
Q9LE39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q27271
Q922X1
Q9X8F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q15456
Q26209
Q26213
Q9KDC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            018822
Q9TTD6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09APQ5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     002801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                               sp_humān:*
sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of res
score greater than or equal to
and is derived by analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_mhc:*
sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  П
                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
                                                                                                                              US-09-696-169A-20
277
                                                                                                                                                                                                                                                                                                                                                             sp_archea:*
sp_bacteria:*
sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110
110
110
116
116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_archeap:
                                                                                                                                                                                                                                                                                                                                                                                                                         sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_plant:*
                                                                                                                                                                                                                                                                                                                                                   SPTREMBL_19:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4458644884448888444988
                                                                                                                                                                                                                                                               length: 0
length: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1155.9
1175.9
1175.1
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
1177.7
11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10:
112:
123:
14:
176:
                                                                                                                                                                                                                                          Total number of
                                                                                                                                                                                                                                                                 sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                          Perfect score:
                                                                                                                                                                              Scoring table:
                                                          protein
                                                                                                                                                                                                                                                                Minimum DB
Maximum DB
                                                                                                                                                        Seguence:
                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Result
                                                                                                                               Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š.
```

**Q9LE39** Q9LE39;

7

RESULT

**09LE39** 

```
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20196006; PubMed=10731132;
MEDLINE-20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J. R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CO-92 BIOVAR ORIENTALIS;
Karlyshev A.V., Wren B.W.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ALL17211; Cap. 1990) to the Hypothetical protein; Plasmid.
SEQUENCE 48 AA; 5417 MW; BFD2188AF24BED48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  James K.D., Parkhill J., Barrell B.G., Rajandream M.A., Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 5.4 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 LDEVYNAAYNAADHAAPEDKYEAFVLHFSEALHII 40
                                                                                                                   48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
SEQUENCE FROM N.A.
STRAIN-CO-92 BIOVAR ORIENTALIS;
Baker S.G., Mungall K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CO-92 BIOVAR ORIENTALIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 14.8'
Best Local Similarity 31.4'
Matches 11; Conservative
                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                            Yersinia pestis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CG15353 PROTEIN.
                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=632;
                                                                                                                                                                                                                                                                                Plasmid pMT1.
                                                                                                                                                                                                                                                                                                                        Yersinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09VQ65;
09VQ65;
                                                                                                                   Q9RID3
                                                                                4
                                                                                RESULT
                                                                                                 Q9RID3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                            Glycine max (Soybean).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stronvik M.V., Sundararanan V.P., Vodkin L.O.;
"A novel promoter that is active in a complex developmental pattern with and without its proximal 650 base pairs.";
Plant Mol. Biol. 41:217-231(1999).
EMBL: AJ293442; CAB967661; -..
EMBL; AJ293438; CAB96760.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECUENCE FROM N.A.
MEDLINE=20575196; PubMed=11133432;
Entcheva P., Liebl W., Johann A., Hartsch T., Streit W.R.;
"Direct cloning from enrichment cultures, a reliable strategy for isolation of complete operons and genes from microbial consortia.";
Appl. Environ. Microbiol. 67:89-99(2001).
EMBL; AF250771; AAG60565.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           œ
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.9%; Score 44; DB 10; Length 45; ilarity 31.6%; Pred. No. 1.7e+02; Conservative 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB 2; Length 44; Pred. No. 4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Indels
                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2327E24CEA15458E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 AA; 5262 MW; 6C73B171FDE4F678 CRC64;
                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2011 (TrEMBLrel. 16, Last annotation update)
MAJOR LATEX PROTEIN HOMOLOGUE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 YNAADHAAPE-DKYEAFVLHFSEALHIIAGTPEVHAVK 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 YEKVDHTAPEPTKYKDLVVKLTKNV-----EAHLVE 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CV, CLARK;
MEDLINE-20044090; PubMed-10579489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; environmental samples. NCBI_TaxID=143796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 DEVYNAAYNAADHAAPEDKYEAFV 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uncultured bacterium pCosHE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 37.5%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 AA; 5236 MW;
                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 12; Conserv
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                         STRAIN-CV. CLARK;
Vodkin L.O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELSG (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
SEQUENCE
```

Query Match

Best Loca Matches

ò ДQ Q9APQ5 Q9APQ5;

ŏ

RESULT **09AP05** 

ö

Gaps

ö

Length 48; Indels

```
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Buttlas K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Rad Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA bodson K., Doub L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA boster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Hemiann T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Havey D., Hemiann T.J., Hernandez J.R., Hock J.,
RA Harris N.L., Havey D., Hemiann T.J., Hernandez J.R., Hock J.,
RA Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Rimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merklov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,
RA Palazzolo M., Pittann G.S., Pon S., Pollard J., Puri V., Resee M.G.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Strposk M.P., Sun E.,
Syier E., Spradling A.C., Stapleton M., Strposk M.P., Sinit T.,
RA Stirskas R., Tector C., Turner R., Venter E., Wang S., Yao Q.A.,
RA Hallams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Hallams S.M., Myers E.W., Rubin G.M., Venter J.C.,
R. Sheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu K., Shier F., Sheng R., Sheng R., Sheng Sequence of Incosophila melanogaster F.,
R. Shier S. Shiel S. Smith H.O.,
R. Shier S. Shiel S. Smith H.O.,
R. Shier S. Shiel S. Smith H.O.,
R. Shien S. Shiel S. Smith H.O.,
R. Sheng X.H., Zhong W., Zhong S., Zhu 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=CV. WILLIAMS 82;
TISSUE=SHOOT APEX, 9-10 DAY OLD ETIOLATED SEEDLINGS;
MEDLINE=20044090; PubMed=10579489;
Stromvik M.V., Sundararaman V.P., Vodkin L.O.;
"A novel promoter that is active in a complex developmental pattern with and without its proximal 650 base pairs.";
Plant Mol. Biol. 41:217-231(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosida eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.1%; Score 39; DB 5; Length 53; 45.0%; Pred. No. 9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=CV. WILLIAMS 82;
TISSUE-SHOOT APEX, 9-10 DAY OLD ETIOLATED SEEDLINGS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 AA; 5450 MW; 663595A2F81D2E9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 9e+(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAJOR LATEX PROTEIN HOMOLOGUE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FBgn0040718; CG15353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 287:2185-2195(2000).
EMBL; AE003584; AAF51316.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11: ||:| |:|
31 VPQF--VYSAGYPAVGYASP 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 VPKLDEVYNAAYNAADHAAP 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 45.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycine max (Soybean).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=3847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09LEJ3;
01-OCT-2000 (
01-OCT-2000 (
01-DEC-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L.O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FlyBase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vodkin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9LEJ3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
Q9LEJ3
           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 윤
```

```
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                      Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus
                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98398091; PubMed-9730323;
Wang Y., Westby C.A., Johansen M., Marshall D.M., Granholm Tsolation, cloning, and sequencing of porcine agout1 exon (PorAex2)...;
Pigment Cell Res. 11:155-157(1998).
EMBL; AF018166; AAC34732.1; -.
                                                               Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ٥.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38; DB 6; Length 37;
Pred. No. 8e+02;
                                                                                         indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20292452; PubMed-10834600;
Kim K.S., Mendez E.A., Marklund S., Clutter A.C., Pomp
Rothschild M.F.;
                         4FE1EB734C2C5B4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5555E9CE37DDF6DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 AA; 4447 MW; 7239F4E34CAE419E CRC64;
                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                              Score 38; DB 10;
Pred. No. 6.5e+02;
6; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Linkage mapping of the porcine Agouti gene."; J. Anim. Sci. 78:1395-1396(2000).
                                                                                                                                                                                                             AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 AA
                                                                                                                               || || || || || : : : | | | |: 3 DHTAPEPTKYKDLVVKLTKNV-----EAHLVE 29
                                                                                                                  18 DHAAPE-DKYEAFVLHFSEALHIIAGTPEVHAVK 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                            37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF133261; AAF22158.1; -. NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.7%;
50.0%;
                                                             Query Match 13.7%;
Best Local Similarity 32.4%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 AA; 4100 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                         31 AA; 3530 MW;
EMBL; AJ293444; CAB96765.1;
                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGOUTI (FRAGMENT).
Sus scrofa (Pig).
                                                                                                                                                                                                                                                                          AGOUTI (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-YORKSHIRE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : |: | |||:|
10 FTASSHLAPEEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 YNAADHAAPEDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40
                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9823
            NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
                                                                                                                                                                                                         018822 018822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O9TTD6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9TTD6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                               018822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9TTD6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . අ
                                                                                                                                          g
PT
SQ
                                                                                                                                                                                                            ò
```

```
Query Match
Best Local Similarity
Matches 7; Conserv
 50
50 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                 NCBI_TaxID=382;
 NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCE39.28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9X8F1
Q9X8F1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
                                                                                                                                RESULT 11
                                                                                                                                           Q922X1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09X8F1
                                                                                 ò
                                                                                                                                                               ö
                              ö
                              Gaps
                                                                                                                                                                                                                                                               A3(2) that resemble the major class of motility-related promoters in J. Bacteriol. 175:933-940(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Borre M.B., Owen C.A., Keen J.K., Sinha K.A., Holder A.A.; "Multiple genes code for high-molecular-mass rhoptry proteins of Plasmodium yoelii.";
                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium berghei yoelii.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5862;
Score 38; DB 6; Length 40;
Pred. No. 8.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 34.6%; Score 38; DB 2; Length 48; Similarity 34.6%; Pred. No. 1.1e+03; 9; Conservative 6; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                  STRAIN=A3(2);
Bruton C.J.;
Bruton C.J.;
Submitted (OCT-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; X68791; CAA48686.1;
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                 0F2D3913881B1735 CRC64;
                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HYPOTHETICAL PROTEIN IN PTH4 PROMOTER (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
RHOPTRY PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol. Blochem. Parasitol. 70:149-155(1995).
EMBL; U19985; AAC46620.1; -.
EMBL; U19979; AAC46614.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 AFVLHFSEALHIIAGTPEVHAVKPGA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95364832; PubMed=7637695;
                                                                                                                                                                                                                                            STRAIN-A3(2);
MEDLINE-93163057; Pubmed-7679386;
       13.7%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 48 AA; 4815 MW;
                             6; Conservative
                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                 Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                       48
                                                            : |: | |||:|
5 FTASSHLAPEEK 16
                                                14 YNAADHAAPEDK 25
         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sest Local Similarity
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=YM;
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                     Q02801
Q02801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           027271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
Q27271
                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                   qq
                                                                                                                               õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     õ
```

```
ö
                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
Gurjal M., Hong A., Hulzar L., Hyman R.W., Kahn D., Kahn M.L.,
Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
"Nucleotide sequence and predicted functions of the entire
                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid pSymA (megaplasmid 1).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                        ;;
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.7%; Score 38; DB 16; Length 53; 41.2%; Pred: No. 1.2e+03; Artive 2; Mismatches 8; Indels
                                                                                                                                                                                                                 2 LVPKLDEVYNAAYNAADHAAPEDKYEAFVLHFSEALHIIAGTPEVHAVK 50
                                                                                                                                                                                                                                                       Ouery Match 13.7%; Score 38; DB 5; Length 50; Best Local Similarity 24.5%; Pred. No. 1.1e+03; Matches 12; Conservative 13; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=A3(2); Oliver K., Harris D.; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AE007225; AAK64985.1; -.
Hypothetical protein; Plasmid; Complete protecome.
SEQUENCE 53 AA: 5568 MW; 40316BEA492AB2DB CRC64;
6042 MW; 33B9D1EA07A4265E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHEFICAL PROTEIN SMA0625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 4.2 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sinorhizobium meliloti pSymA megaplasmid.";
Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
EMBL; AE007225; AAK64985.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                  53 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhizobium meliloti (Sinorhizobium meliloti).
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=1021;
MEDLINE=21396509; Pubmed=11481432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 AFVLHFSEALHIIAGTP 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 AFMLFLQSVVHAFAGQP 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
```

```
Eukaryota; Álveolata; Apicomplexa; Haemosporida; Plasmodium
NCBI_TaxID=5861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: July 11, 2002, 11:03:43 Job time: 205 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=YM;
       Plasmodium yoelii.
                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U199
NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                       026213
                                                                                                                                                                                                                                                                                                                                                            026213
                                                                                                                                                                                                                                                                                                                                     RESULT 15
                                                                                                                                                                                                                                                                                                                                               026213
                                                                                                                                                                                                                                                                                              pp
      Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schultz S.J., Nigg E.A.; "Identification of 21 novel human protein kinases, including 3 members of a family related to the cell cycle regulator nimA of Aspergillus nidulans."
                                                                                       Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL049573; CAB40336.1;
Hypothetical protein.
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
STRAIN=A3(2);
Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                   13.4%; Score 37; DB 2; Length 42; 58.3%; Pred. No. 1.3e+03; tive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.4%; Score 37; DB 4; Length 46; ilarity 34.5%; Pred. No. 1.4e+03; Conservative 2; Mismatches 17; Indels
                                                                                                                                                                               42 AA; 4168 MW; 999E9AABE3EA1500 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 46
46 AA; 5140 MW; 66C551D29D7382D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROTEIN-SERINE THREONINE KINASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                          46 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00069; pkinase; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 YNAADHAAPEDKYEAFVLHFSEALHIIAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell Growth Differ. 4:821-830(1993)
EMBL, 225435; CAA80922.1; -.
InterPro; IPR000719; Euk_pkinase.
                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                               STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-94100173; PubMed=8274451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP-binding; Kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19, RHOPTRY PROTEIN (FRAGMENT).
                                                                                                                                                                                                                               Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                     42 GTPEVHAVKPGA 53
                                                                                                                                                                                                                                                                                           8 GVPSRHAVREGA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 10; Conserva
                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 026209;
                                                                                                                                                                                                                                                                                                                                                         015456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
Q26209
ID Q26209
AC Q26209,
DT 01-NOV.
DT 01-DEC.
DE RHOPTR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    026209
                                                                                                                                                                                                                                                                                                                                 RESULT 13
Q15456
     ò
                                                                                                                                                                                                                                                                                                                                                         Op
```

```
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                      Gaps
MEDLINE=95364832; PubMed=7637695;
Borre M.B., Owen C.A., Keen J.K., Sinha K.A., Holder A.A.;
"Multiple genes code for high-molecular-mass rhoptry proteins of
Plasmodium yoelii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Borre M.B., Owen C.A., Keen J.K., Sinha K.A., Holder A.A.;
"Multiple genes code for high-molecular-mass rhoptry proteins of
Plasmodium yoelii.";
Mol. Biochem. Parasitol. 70:149-155(1995).

EMBL; U19987; AAC46622.1; -.
                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Ālveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5861;
                                                                                                                                                                                                                                                                               Query Match 13.4%; Score 37; DB 5; Length 50; Best Local Similarity 25.6%; Pred. No. 1.5e+03; Matches 10; Conservative 12; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.4%; Score 37; DB 5; Length 50; 25.6%; Pred. No. 1.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15; Indels
                                                                                                                                                                                  50 50
50 AA; 6023 MW; C378C78A42AA43C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 AA; 6050 NW; F801F78A42AA5848 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                  2 LVPKLDEVYNAAYNAADHAAPEDKYEAFVLHFSEALHII 40
                                                                                                                                                                                                                                                                                                                                                                                                              2 LVPKLDEVYNAAYNAADHAAPEDKYEAFVLHFSEALHII 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Mismatches
                                                                                          Mol. Biochem. Parasitol. 70:149-155(1995).
EMBL; U19980; AAC46615.1; -.
NON_TER 1 1
SEQUENCE 50 AA; 6023 MW; C378C78A42AA4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95364832; PubMed=7637695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RHOPTRY PROTEIN (FRAGMENT).
Plasmodium yoelii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 25.69
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
```

ĕ

```
Kentucky Blue Gras
LPIX-10, peptide f
LPIX-9, peptide fr
LPIX-11, peptide f
LPIX-12, peptide f
Kentucky Blue Gras
LPIX-13, peptide f
Kentucky Blue Gras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1980.DAT:*
2; /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:*
3: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:*
4: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:*
5: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:*
6: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1986.DAT:*
7: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1986.DAT:*
8: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1980.DAT:*
9: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1980.DAT:*
10: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1980.DAT:*
11: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1990.DAT:*
12: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1992.DAT:*
13: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1992.DAT:*
14: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1994.DAT:*
15: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1995.DAT:*
16: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1995.DAT:*
17: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1995.DAT:*
18: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1995.DAT:*
18: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1995.DAT:*
18: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1995.DAT:*
18: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1995.DAT:*
18: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1995.DAT:*
19: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1995.DAT:*
18: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1995.DAT:*
18: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1995.DAT:*
18: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1995.DAT:*
                                                                                                July 11, 2002, 10:56:43; Search time 29.64 Seconds (without alignments) 198.614 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1997.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1998.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               number of results predicted by chance to have a no or equal to the score of the result being printed, analysis of the total score distribution.
                                                                                                                                                                                                                  53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                .....SEALHIIAGTPEVHAVKPGA
                                                                                                                                                                                                                                                                                                                                                362426
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                              hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                          747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Listing first 45 summaries
                                                                      protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR89393
AAR71517
AAR71516
AAR71518
AAR71519
AAR89392
AAR89391
AAR89391
AAR89391
AAW76473
AAW76473
                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                QLVPKLDEVYNAAYNAADHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A_Geneseq_032802:*
1; /srr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   than or equal to
by analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1
                                                                                                                                                                            US-09-696-169A-20
277
                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 08
Maximum Match 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117
116
116
117
119
119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length: 0
length: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  re greater than is derived by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  255.3
200.6
200.6
200.6
17.7
17.3
15.9
15.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oţ
                                                                                                                                                                                                                                                                                                                                                                                    sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70
55
57
54
44
44
44
                                                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                      •
                                                                                                                                                                                                                                                                                                                                              Total number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   score and is
                                                                                                                                                                                                                                                                                                                                                                                  0B
0B
                                                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                                                                                                                                                                                                                                                                                                                  Minimum
                                                                                                                                                                                                                                                                                                                                                                                                     Maximum
                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3
4
4
7
7
10
10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  М
М
```

Graminae pollen al LPIX-5, peptide fr Kentucky Blue Gras Cationic peptide a Cationic peptide A E. coli AMP gene a Physcomitralla pat

Peptide #9114 enco Protein #7433 enco Human brain expres Peptide #6993 enco Peptide #9438 enco Human prostate can Human CYP2B6 prote Human CYP2B6 prote

AAB51195 AAB99854

AAY91693

AAW66394

ABB41608

Human bone marrow

ABB25434 AAM62479 AAM75288 AAM20559

AAM35401 AAB56544 AAU06521

AAU06522

ALIGNMENTS

RESULT

Staphylococcus aur Human secreted pro

AAB32429 AAW76484 AAR71512 AAR89394

Graminae pollen al Insulin 1 B-chain.

Peptide #1174 enco Peptide #1200 enco Peptide #1144 enco LPIX-6, peptide fr Novel human diagno Amino acid residue

AAM27163 AAM02462

AAR71513

ABG27510 AAY42432 AAW76486 AAW47366 AAW79410

Integrin alpha-6a Peptide #1171 enco Peptide #1211 enco Protein #1153 enco

AAW10860 AAR80961 ABB28520 ABB33705

ABB19154 AAM54473

AAM66878 AAM14740

115.9 115.9

Human brain expres

anti-HBSAg bin anti-HBSAg bin

Peptide including at least 1 human antigenic determinant of Kentucky Blue Grass allergen - from Poa p IX  $gp.\ of\ grass\ pollen\ allergens,$ Antigenic determinant; recombinant; Kentucky Blue Grass; pollen; allergen; antigenic; rKBG60; Poa p IX group; desensitisation; allergic; allergy; prevention; development; reaction; grass; antibody; anergise; producing cell; diagnosis; human; clone 60; immunological response; B-cell; hIgG; hIgE; T-cell. Kentucky Blue Grass pollen allergen rKBG60 resides 129-148. Æ AAR89393 standard; peptide; 20 95WO-CA00439 94US-0280455 17-SEP-1996 (first entry) (UYMA-) UNIV MANITOBA WPI; 1996-116753/12. Poa pratensis WO9603106-A2 26-JUL-1995; 26-JUL-1994; Mohapatra SS; 08-FEB-1996 AAR89393; AAR89393 glutamicum prote raminae pollen al

C glutamio Graminae j Graminae Length 20;

DB 16;

```
02-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 LVPKLDEVYNAAYNAAD 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:|||| |: || ||:
3 lipkldtaydvaykaae 19
                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Griffith IJ, Kuo M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-115444/15
                                                                                                                                                                                                                                                                            perenne; Lol
                           Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR71518 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 AA;
                                                                                                                                                                                                                                                                                                                                                                                            05-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                     13-AUG-1993;
                                                                                                                                                                                                                          02-NOV-1995
                                                                                                                                                                                                                                                                                                                                           WO9506728-A.
                                                                                                                                                                                                                                                                                                                                                                    09-MAR-1995
                                                                                                                                                                                                AAR71516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR71518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
AAR71518
                                                                                                         g
                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lol pV, is a major allergen of ryegrass pollen, and is encoded by the CDNA sequence of clone 12R (AAQ85932), a full-length clone derived from a lambda gill library. Peptides (AAR71508-61) comprising at least one T cell epitope derived from the Lol pV protein are claimed, and can be used to treat or diagnose sensitivity to ryegrass pollen in an individual or to pollen proteins that are immunologically related to Lol pV, such as Dac gV (see AAR71507).
                                                                                                                                                                                                                                                                                         Gaps
                                                           The present peptide is a human antigenic determinant contg. peptide, compprising residues 129-148 of the recombinant Kentucky Blue Grass pollen allergen rKBG60, which is from the Poa p IX 9P. of grass pollen allergens. A compsn. comprising the peptide and a carrier can be used to desensitise allergic individuals, and prevent allergic Individuals from developing an allergic reaction to grass pollen. The compsn. may also be used to deplete allergen specific antibody producing cells. The peptide can be used to diagnose grass pollen allergy, and has the following human immunological response profile, B-cell (hIgG (-)/hIgE (-)), T-cell (-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lolium perenne Lol pV and Dactylis glomerata Dac gV epitope(s) and DNA - for treating sensitivity to rye-grass pollen allergen or an immunologically cross-reactive allergen.
used to desensitise allergic individuals, prevent grass pollen allergy and deplete allergen-specific antibodies
                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lolium perenne; Lol pV; Dactylis glomerata; Dac gV; epitope;
                                                                                                                                                                                                                                                           Score 70; DB 17; Length 20;
Pred. No. 0.0073;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide fragment of Lol pV protein allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sensitivity; ryegrass pollen allergen.
                                                                                                                                                                                                                                                                                                                                                                                                         ¥.
                                      Example 5; Page 29; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lugman M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 2; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                      AAR71517 standard; Protein; 20
                                                                                                                                                                                                                                                            25.3%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IMMU-) IMMULOGIC PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93US-0106016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94WO-US09024
                                                                                                                                                                                                                                                                                                                             34 SEALHIIAGTPEVHAVKP 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                       15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-115444/15.
                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                       20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lolium perenne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Griffith IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9506728-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-MAR-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                AAR71517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                       Matches
ò
                                                                                                                                                                                                                                                                                                                                        g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lol pV, is a major allergen of ryegrass pollen, and is encoded by the CDNA sequence of clone 12R (AAQ85932), a full-length clone derived from a lambda gtll library. Peptides (AAR71508-61) comprissing at least one T cell epitope derived from the Lol pV protein are claimed, and can be used to treat or diagnose sensitivity to ryegrass pollen in an individual or to pollen proteins that are immunologically related to Lol pV, such as Dac gV (see AAR71507).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lolium perenne Lol pV and Dactylis glomerata Dac gV epitope(s) and DNA - for treating sensitivity to rye-grass pollen allergen or an immunologically cross-reactive allergen.
                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pv; Dactylis glomerata; Dac gv; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 16; Length 20;
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LPIX-9, peptide fragment of Lol pV protein allergen.
23.5%; Score 65; DB 16 60.0%; Pred. No. 0.036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 57; DB 16
Pred. No. 0.47;
3; Mismatches
                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sensitivity; ryegrass pollen allergen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 AA.
                                                                                                                                                                                                                                                                                                         AAR71516 standard; Protein; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lugman M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 2; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.6%;
58.8%;
                                                                                                                                            |: || ||: | || ||:||
| ydvaykaaegatpeakydaf 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IMMU-) IMMULOGIC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93US-0106016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                            10 YNAAYNAADHAAPEDKYEAF
```

```
LOI PV, 1S a major allergen of ryegrass pollen, and is encoded by the CDNA sequence of clone 12R (AAQ85932), a full-length clone derived from a lambda gtll library. Peptides (AAR71508-61) comprising at least one real epitope derived from the Lol pv protein are claimed, and can be used to treat or diagnose sensitivity to ryegrass pollen in an individual or to pollen proteins that are immunologically related to Lol pv, such as Dac gV (see AAR71507).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide including at least 1 human antigenic determinant of Kentucky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present peptide is a human antigenic determinant contg. peptide, comprising residues 109-128 of the recombinant Kentucky Blue Grass pollen allergen rKBG60, which is from the Poa p IX gp. of grass pollen allergens. A compsn. comprising the peptide and a carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blue Grass allergen - from Poa p IX gp. of grass pollen allergens, used to desensitise allergic individuals, prevent grass pollen allergy and deplete allergen-specific antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antigenic determinant; recombinant; Kentucky Blue Grass; pollen; allergen: antigenic; rKBG60; Poa p IX group; desensitisation; allergy; prevention; development; reaction; grass; antibody; anergise; producing cell; diagnosis; human; clone 60; immunological response; B-cell; hIgG; hIgE; T-cell.
                                                                        Lolium perenne Lol pV and Dactylis glomerata Dac gV epitope(s) and DNA - for treating sensitivity to rye-grass pollen allergen or an immunologically cross-reactive allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kentucky Blue Grass pollen allergen rKBG60 resides 109-128
                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                           Score 54; DB 16;
Pred. No. 1.2;
2; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; Page 29; 59pp; English.
Luqman M;
                                                                                                                                                      Claim 1; Fig 2; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR89392 standard; peptide; 20
                                                                                                                                                                                                                                                                                                                                                                                                               19.5%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94US-0280455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 VLHFSEALHIIAGTPEVHAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-SEP-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYMA-) UNIV MANITOBA
  Kuo M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-116753/12.
                                    WPI; 1995-115444/15
                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                     20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pratensis
Griffith IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9603106-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mohapatra SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-FEB-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR89392;
                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Poa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lol pV, is a major allergen of ryegrass pollen, and is encoded by the DNA sequence of clone 12R (AAQ8592), a full-length clone derived from a lambda gill library. Peptides (AAR71508-61) comprising at least one T cell epitope derived from the Lol pV protein are claimed, and can be used to treat or diagnose sensitivity to ryegrass pollen in an individual or to pollen proteins that are immunologically related to Lol pV, such as Dac gV (see AAR71507).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                Lolium perenne Lol pV and Dactylis glomerata Dac gV epitope(s) and DNA - for treating sensitivity to rye-grass pollen allergen or an immunologically cross-reactive allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                      Lolium perenne; Lol pV; Dactylis glomerata; Dac gV; epitope; sensitivity; ryegrass pollen allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dac gV; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.2%; Score 56; DB 16; Length 20; 55.0%; Pred. No. 0.65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Indels
                LPIX-11, peptide fragment of Lol pV protein allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPIX-12, peptide fragment of Lol pV protein allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lolium perenne; Lol pv; Dactylis glomerata; sensitivity; ryegrass pollen allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR71519 standard; Protein; 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 2; 110pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | || || :||| :||| :|| :| atpeakydafvtaltealrv 20
                                                                                                                                                                                                                                                                                                             (IMMU-) IMMULOGIC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 AAPEDKYEAFVLHFSEALHI 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IMMU-) IMMULOGIC PHARM CORP
                                                                                                                                                                                                                                   94WO-US09024.
                                                                                                                                                                                                                                                                       93US-0106016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94WO-US09024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93US-0106016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Conservative
                                                                                                                                                                                                                                                                                                                                                   Griffith IJ, ' Kuo M,
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-115444/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 AA;
                                                                                                                Lolium perenne.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lolium perenne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-AUG-1994; ,
                                                                                                                                                                                                                                                                       13-AUG-1993;
                                                                                                                                                                                                                                   05-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-NOV-1995
                                                                                                                                                    W09506728-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9506728-A.
                                                                                                                                                                                          09-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR71519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
```

Matches

AAR71519

a

ò

ö

Gaps

;

Indels

(first entry)

888888888888

ð ద

```
Antigenic determinant; recombinant; Kentucky Blue Grass; pollen;
                                                                                                                                                                                                                                 allergen; antigenic; rKBG60; Poa p IX group; desensitisation; allergic; allergy; prevention; development; reaction; grass; antibody; anergise; producing cell; diagnosis; human; clone 60; immunological response; B-cell; hIgG; hIgE; T-cell.
                                                                                                                                                                              Kentucky Blue Grass pollen allergen rKBG60 resides 99-118.
                                                                        AAR89391 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYMA-) UNIV MANITOBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-116753/12.
                                                                                                                                                                                                                                                                                                                       Poa pratensis
                                                                                                                                                                                                                                                                                                                                                        WO9603106-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mohapatra SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                          26-JUL-1995;
                                                                                                                                              17-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                           08-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence
                                                                                                           AAR89391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                        œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loc
Matches
                                        RESULT
AAR89391
                                                                                           à
                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lol pv, is a major allergen of ryegrass pollen, and is encoded by the cDNA sequence of clone 12R (AAQ85932), a full-length clone derived from a lambda gtll library. Peptides (AAR71508-61) comprising at least one T cell epitope derived from the Lol pv protein are claimed, and can be used to treat or diagnose sensitivity to ryegrass pollen in an individual or to pollen proteins that are immunologically related to Lol pv, such as Dac gV (see AAR71507).
                                                                                                                                                                                                                                   Gaps
can be used to desensitise allergic individuals, and prevent allergic individuals from developing an allergic reaction to grass pollen. The compsn. may also be used to deplete allergen specific antibodies from an individual, and anergise allergen specific antibody producing cells. The peptide can be used to diagnose pollen allergy, and has the following human immunological response profile, B-cell (hIgG (-)/hIgE (-)), T-cell (+).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lolium perenne Lol pV and Dactylis glomerata Dac gV epitope(s) and DNA - for treating sensitivity to rye-grass pollen allergen or an immunologically cross-reactive allergen.
                                                                                                                                                                                                                                 .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lolium perenne; Lol pV; Dactylis glomerata; Dac gV; epitope; sensitivity; ryegrass pollen allergen.
                                                                                                                                                                                             Score 49; DB 17; Length 20; Pred. No. 6.2;
                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPIX-13, peptide fragment of Lol pV protein allergen.
                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         AAR71520 standard; Protein; 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 2; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IMMU-) IMMULOGIC PHARM CORP.
                                                                                                                                                                                               17.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94WO-US09024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93US-0106016
                                                                                                                                                                                                                                                                    13 AYNAADHAAPEDKYEAFV 30
                                                                                                                                                                                                                                                                                        || :|: | || ||: :|
| ayksaegatpeakyddyv 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-NOV-1995 (first entry)
                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kuo M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-115444/15.
                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                            20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lolium perenne.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Griffith 1J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9506728-A.
                                                                                                                                                                                                                                   .
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAR-1995
                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                          AAR71520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                        RESULT
AAR71520
```

94US-0280455.

```
ö
Peptide including at least 1 human antigenic determinant of Kentucky Blue Grass allergen - from Poa p IX gp. of grass pollen allergens, used to desensitise allergic individuals, prevent grass pollen allergy and depter ellergen-specific antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                  The present peptide is a human antigenic determinant contg. peptide, comprising residues 99-118 of the recombinant Kentucky Blue Grass pollen allergen rKBGGO, which is from the Poa p IX qp. of grass pollen allergens. A compos. comprising the peptide and a carrier can be used to desensitise allergic individuals, and prevent allergic individuals from developing an allergic reaction to grass pollen. The compsn. may also be used to deplete allergen specific antibody producing cells. The peptide can be used to diagnose grass poilen allergy, and has the following human immunological response profile, B-cell (hIGG (-)/hIGE (+)), T-cell (+).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.0%; Score 47; DB 17; Length 20; 50.0%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 AA.
                                                                                                                                        Claim 7; Page 29; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG93042 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 KLDEVYNAAYNAADHAAP 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG93042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG93042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      £
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            XXXXXX
```

ó

Gaps

.; 0

2; Indels

0; Mismatches

Conservative

Query Match Best Local Similarity Matches 10; Conserv

ò g

Score 48; DB 16; Length 20; Pred. No. 8.5;

17.3%; 83.3%;

ij

Jaeger

```
AAW76449-W76534 are peptide fragments of a natural pollen allergen, Phl p 5b, isolated from Graminae species. This allergen can be modified and the reactivity of the modified allergens with IgE antibodies to grass pollen allergens is reduced or eliminated while their reactivity with T cells is retained. The genes for the allergens are modified so that the encoded polypeptides have one or more amino acid substitutions, deletions and/or additions. The dominant T-cell epitopes of the allergens are not genetically altered. Such allergens have applications in the immunotherapy of allergies e.g. hyposensitisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pollen; allergen; Phl p 5b; IgE; antibody; grass; reactivity; T cell; epitope; immunotherapy; allergy; hyposensitisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified recombinant allergens - useful for immuno-therapy of
                                                                                                                                                                                                                                                                                  Modified recombinant allergens - useful for immuno-therapy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.9%; Score 44; DB 19; Length 12; 66.7%; Pred. No. 16; 3; Indels iive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Graminae pollen allergen Phl p 5b peptide fragment #37
                                                                                                                                                                                      Fiebig H, . Stuewe H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fiebig H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mueller W, Schramm G,
                                                                                                                                                                                      Cromwell O, F
W, Schramm G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW76485 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                        Example 1; Page 12; 31pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cromwell O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97DE-1013001.
                                                                         97DE-1013001
                                                                                                              97DE-1013001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97DE-1013001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MERE ) MERCK PATENT GMBH.
                                                                                                                                                 (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                        Bufe A, (Mueller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 VPKLDEVYNAAY 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||||| |: ||
| vpkldaaysvay 12
                                                                                                                                                                                                                                               WPI; 1998-522170/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-522170/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bufe A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 AA;
DE19713001-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DE19713001-A1
                                                                     27-MAR-1997;
                                                                                                              27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-MAR-1997;
                                      01-0CT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1998
                                                                                                                                                                                      Becker W,
Kahlert H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kahlert H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Becker W,
                                                                                                                                                                                                                                                                                                       allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Graminae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW76485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW76485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel polynucleotides derived from Coryneform bacteria, for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pollen; allergen; Phl p 5b; IgE; antibody; grass; reactivity; T cell; epitope; immunotherapy; allergy; hyposensitisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                         Ochiai K, Yokoi H;
                                    Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 17; SEQ ID NO: 6796; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Graminae pollen allergen Phl p 5b peptide fragment #25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAADHAAPEDKYEA-----FVLHFSEALHIIAGTPEVHAV
                                                                                                                                                                                                                                                                                                                                                         Hayashi M,
C glutamicum protein fragment SEQ ID NO: 6796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44.5;
Pred. No. 89;
                                                                                                                                                                                                                                                                                                                                                                             Ozaki A;
                                                                                                                                                                                                                                                                                                                                                           Ando S,
                                                                                                                                                                                                                                                                                                                                                                         Ikeda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW76473 standard; peptide; 12
                                                                                                                                                                                                                                         99JP-0377484.
2000JP-0159162.
2000JP-0280988.
                                                                                                                                                                                                                                                                                                                      (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.1%;
35.7%;
                                                                                                                                                                                                      18-DEC-2000; 2000EP-0127688.
                                                                                           Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                        organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                         Mizoquchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European Patent Office
                                                                                                                                                                                                                                                                                                                                                                             Senoh A,
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-376931/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAH68261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 AA;
                                                                                                                                                                                                                                           16-DEC-1999;
07-APR-2000;
03-AUG-2000;
                                                                                                                              EP1108790-A2
                                                                                                                                                                                                                                                                                                                                                         Nakagawa S,
Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-DEC-1998
                                                                                                                                                                     20-JUN-2001
```

Sequence

AAW76473,

AAW76473

~

g

Graminae

ö

Gaps

ö

Jaeger

Stuewe H;

```
limiting amount of an affinity receptor for the analyte. The conjugate exhibits an activity that is altered upon interaction with the affinity receptor and this activity can be measured and related to the amount of the analyte present in a sample. Functional surrogates such as this have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CYTO-) CYTOGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-077284/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAT48656.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9641172-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carter JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW10860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW10860
  555555555555555555555<del>x</del>8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db
                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Functional surrogate; analyte; affinity receptor; immunoreactive group; mimic; homogenous immunoassay; detection; diagnostic analyte; Chlamydia; cardiac marker; tumour marker; allergen; hormone; fertility; myoglobh; pregnancy; infectious disease; ferritin; myosin light chain; troponin; follicle stimulating hormone; human; growth hormone; immunoglobulin E; prolactin; parathyroid hormone; placental lactogen; hepatitis antigen; antibody; chorionic gonadotropin; luteinising hormone; cytomegalovirus; Streptococcus; rubella; toxoplasma; DK-MB; prostate-specific antigen; carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125.
                                                                  phl p 5b, isolated from Graminas species. This allergen can be modified and the reactivity of the modified allergens with IgE antibodies to grass pollen allergens is reduced or eliminated while their reactivity with T cells is retained The genes for the allergens are modified so that the encoded polypeptides have one or more amino acid substitutions, deletions and/or additions. The dominant T-cell epitopes of the allergens are not genetically altered. Such allergens have applications in the immunotherapy of allergies e.g. hyposensitisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a monoclonal anti-hepatitis B antigen binder sequence from the R26 library which may be used in the conjugate of the 'invention. The novel labelled conjugate comprises at least one label attached to a functional surrogate of an analyte of interest. The surrogate is capable of competing effectively with the analyte for a
                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Labelled functional surrogate of an analyte - useful as competitor molecule in affinity assays, esp. for detecting large macromolecules such as ferritin
                                                        AAW76449-W76534 are peptide fragments of a natural pollen allergen,
                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                            Score 44; DB 19; Length 12;
Pred. No. 16;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAb anti-HBsAg binder sequence, FC22, from R26 library.
                                                                                                                                                                                                                                                                                                                                                                                                     AAW10845 standard; peptide; 29 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 51; Page 95; 156pp; English.
                            Example 1; Page 12; 31pp; German.
                                                                                                                                                                                                                                          15.9%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96WO-US10498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-0476375
                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-NOV-1997 (first entry)
                                                                                                                                                                                                                                          Query Match 15.9°
Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lee-Own FV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CYTO-) CYTOGEN CORP.
                                                                                                                                                                                                                                                                                                                    :||| ||||||
1 viagalevhavk 12
                                                                                                                                                                                                                                                                                                    39 IIAGTPEVHAVK 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-077284/07
                                                                                                                                                                                                  12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09641172-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carter JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW10845;
                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                        AAW10845
                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                      diagnostic analytes for detection include cardiac or tumour markers, allergens, hormones related to fertility-pregnancy or analytes associated with infectious disease. In particular, the assays are useful for detecting ferritin, follicle stimulating hormone, human growth hormone, immunoglobulin E, prolactin, parathyroid hormone, human placental lactogen, hepatitis antigens or antibodies against them, human choining gonadotropin, human luteinising hormone, cytomegalovirus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydia, Streptococcus a, rubella, toxoplasma, herpes virus, DK-MB, myoglobin, myosin light chain, troponin, carcinoembryonic antigen, alpha-fetoprotein, prostate-specific antigen and CA125 (a tumour marker).
the analyte present in a sample. Functional surrogates such as this have an immunoreactive group that allows the surrogate to compete effectively and with the analyte for a limiting amount of its affinity receptor. Functional surrogates are able to mimic naturally occurring analytes. They can be labelled for use in standard competitive affinity assays (esp. homogenous immunoassays) for detecting large macromolecules such as polypeptides, polysaccharides, polyuclectides, glycoproteins and lipid-containing macromolecules, as well as small haptens. Typical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Functional surrogate; analyte; affinity receptor; immunoreactive group; mimic; homogenous immunoassay; detection; diagnostic analyte; Chlamydia; cardiac marker; tumour marker; allergen; hormone; fertility; myoglobin; pregnancy; infectious disease; ferritin; myosin light chain; troponin; follicle stimulating hormone; human; growth hormone; immunoglobulin E; prolactin; parathyroid hormone; placental lactogen; hepatitis antigen; antibody; chorionic gonadotropin; luteinising hormone; cytomegalovirus; streptococcus; rubella; toxoplasma; DK-MB; prostate-specific antigen; carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Labelled functional surrogate of an analyte - useful as competitor molecule in affinity assays, esp. for detecting large macromolecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 18; Length 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAb anti-HBsAg binder sequence, FC22, from R26 library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.9%; Score 44; DB 38.1%; Pred. No. 49; ive 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW10860 standard; peptide; 33 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96WO-US10498.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95US-0476375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 eidpfyhpiysaadggarsde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 KLDEVYNAAYNAADHAAPEDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 15.9
Best Local Similarity 38.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lee-Own FV;
```

```
The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting
                                                                                                                                                    transmembrane domains of a reporter integrin (RI) fused to the cytoplasmic domain of a target integrin (TI). The RI is pref. from alphanic domain of a target integrin (TI). The RI is pref. from alphal-beta3 and the TI is pref. chosen from alphaV-beta3, alphan-beta2, alpha1-beta1, alpha5-beta1, alpha5-beta1, alpha6-beta1, alpha6-beta1, alpha1-beta3 or alpha4-beta1. This sequence is the cytoplasmic domain of alpha-2. The chimeric integrins are useful for identifying TI inhibitors which can be used to treat mammalian cancers, thrombosis or any unwanted immune respone, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide #1171 encoded by breast cell single exon nucleic acid probe.
Chimeric integrin mol. comprising reporter and target integrin domains - for identifying integrin activation inhibitors which are useful for treating or preventing unwanted immune responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for measuring gene expression in sample derived from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New spatially-addressable set of single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 27; SEQ ID NO 11488; 327pp + sequence listing; English.
                                                                                                                                    Chimeric integrin molecules comprising the extracellular and
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 16; Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         breast, comprises number of single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43.5;
Pred. No. 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ŗ,
                                                                                        Disclosure; Figure 2; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB28520 standard; Peptide; 53 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
                                                                                                                                                                                                                                                                                                                                         inflammation; autoimmune disea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.7%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0180312
2000US-0207456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0632366
2000US-0234687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0608408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0236359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 YNAAYNAAD-HAAPEDK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 ydatyhkaeihagpsdk 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
'-hac 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-496933/54
                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200157271-A2
                                                                                                                                                                                                                                                                                                                                                                                     36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB28520;
                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB28520
  QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                Functional surrogates are able to minimize naturally occurring analytes.
They can be labelled for use in standard competitive affinity assays (esp. homogenous immunoasays) for detecting large macromolecules such as polypeptides, polysaccharides, polynucleotides, glycoproteins and lipid-containing macromolecules, as well as small haptens. Typical diagnostic analytes for detection include cardiac or tumnour markers, with infectious disease. In particular, the assays are useful for detecting ferritin, follicle stimulating hormone, human growth hormone, immunoglobulin E, prolactin, parathyroid hormone, human placental lactogen, hepatitis antigens or antibodies against them, human lactogen, contonic gonadotropin, human luteinising hormone, cytomegalovirus,
                                                                                                                                                                         surrogate is capable of competing effectively with the analyte for a limiting amount of an affinity receptor for the analyte. The conjugate exhibits an activity that is altered upon interaction with the affinity receptor and this activity can be measured and related to the amount of the analyte present in a sample. Functional surrogates such as this have an immunoreactive group that allows the surrogate to compete effectively and with the analyte for a limiting amount of its affinity receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlamydia, Streptococcus a, rubella, toxoplasma, herpes virus, DK-MB, myoglobin, myosin light chain, troponin, carcinoembryonic antigen, alpha-fetoprotein, prostate-specific antigen and CA125 (a tumour marker).
                                                                                   This sequence represents a monoclonal anti-hepatitis B antigen binder sequence from the R26 library which may be used in the conjugate of the invention. The novel labelled conjugate comprises at least one label attached to a functional surrogate of an analyte of interest. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Integrin; chimeric; extracellular; transmembrane; cytoplasmic; ligand; activation inhibitor; inflammation; autoimmune disease; transplantation; thrombus; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 18;
Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Integrin alpha-6a cytoplasmic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR80961 standard; peptide; 36 AA.
                                            Claim 51; Page 97; 156pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.9%;
38.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95WO-US02885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94US-0214770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 KLDEVYNAAYNAADHAAPEDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-APR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ginsberg MH, O'Toole TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SCRI ) SCRIPPS RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-336977/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
such as ferritin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09525173-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-SEP-1995.
```

Sequence

AAR80961;

RESULT 14 **AAR80961** 

g

á

ij

Gaps

ij

Indels

4,

```
the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid product in a nivention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.WiPo.int/Pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 15.5%; Score 43; DB 22; Length 53; Best Local Similarity 54.5%; Pred. No. 1.4e+02; Matches 12; Conservative 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
       δy
```

Search completed: July 11, 2002, 11:00:14 Job time: 211 sec

qq

```
Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-440-861-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
CITY: BC
  \begin{array}{c} \mathbf{n} \\ \mathbf{
(without alignments) 99.966 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                      QLVPKLDEVYNAAYNAADHA......SEALHIIAGTPEVHAVKPGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
Sequence (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                July 11, 2002, 10:58:53; Search time 12.95 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/RB_COMB.pep:*
/cgn2_6/ptodata/2/iaa/RCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-440-861-13
US-08-440-861-114
US-08-433-854-28
US-08-174-745A-28
US-08-135-947-28
US-08-433-985-28
US-08-433-908B-28
US-08-410-614-28
US-08-410-614-28
US-08-410-614-28
US-08-410-614-28
US-08-410-614-28
US-08-214-770-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -08-178-477B-21
-08-440-861-7
-08-749-526-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -08-440-861-8
-08-900-574-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231628 segs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: 'Minimum Match 0%
|Maximum Match 100%
|Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                               US-09-696-169A-20
1277
1 QLVPKLDEVVNANVNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Potal number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               score:
                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                           OM protein
                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database
                                                                                                                                                                                                                                                                                                                                           Perfect
                                                                                                                                                                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š.
```

```
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                         Sequence 45,
Sequence 45,
Sequence 45,
Sequence 15,
                                                                                                                                                                                                                                                                                     Sequence
Sequence
Sequence
Sequence
Sequence
                                   Sequence
                                                                           Sequence
                                                                                             Sequence
                                                                                                                                 Sequence
                                                                                                                                                     Sequence
                                                                                                                                                                       Sequence
                                                                                                                                                                                         Sequence
                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 65; DB 1; Length 20;
Pred. No. 0.019;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Griffith, Irwin J.
APPLICANT: Kuo, Mei-Chang
APPLICANT: Luqman, Mohammad
TITLE OF INVENTION: T CELL EPITOPES OF RYEGRASS POLLEN
TITLE OF INVENTION: ALLERGEN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Amy E. Mandragouras
REGISTRATION NUBLER: 36,207
REFERENCE/DOCKET NUMBER: 1PC-075 (IMI-040cp)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 12:
             US-08-433-854-25
US-08-114-745A-25
US-08-114-745A-25
US-08-433-885-25
US-08-433-908B-25
US-08-410-614-25
US-09-099-307-3
US-08-110-52A-45
US-08-189-331-45
US-08-471-939-45
US-08-471-939-45
US-08-471-939-45
US-08-471-938-45
                                                                                                                                                                                                                                                                   US-08-942-012B-15
US-08-676-242-3
                                                                                                                                                                                                                                                                                                                           US-07-657-769B-57
                                                                                                                                                                                                                                                                                                         US-09-402-732-3
                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII TEAL
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,861
FILING DATE: 15-MAY-1995
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/106,016
FILING DATE: 31-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandwannin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/08440861
Patent No. 5710126
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.5%; 60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-440-861-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
```

ö

App

Sequence 78.

Sequence

Sequence

·08-936-165A-365

US-08-446-692-37 US-08-488-351A;37

Sequence

US-09-082-279B-1226 US-09-315-304B-1226 US-09-082-279B-784 US-09-315-304B-784

.08-817-926-3

Appl Appl Appl

Sequence

Sequence 1226, Ap Sequence 1226, Ap

Sequence

g

δ

```
Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Griffith, Irwin J.
APPLICANT: Kuo, Mei-Chang
APPLICANT: Kuo, Mei-Chang
APPLICANT: Luqman, Mohammad
TITLE OF INVENTION: T CELL EPITOPES OF RYEGRASS POLLEN
TITLE OF INVENTION: ALLERGEN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIYDE & COCKFIELD
STREET: 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
SOFTWARE: ASCII TRAKE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,861
FTLING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/106,016
FILING DATE: 31-AUG-1993
ATTORNEY AGENT INFORMATION:
NAME: AMMY E. MANDERREN 105-075
REFERENCE/DOCKET NUMBER: 1PC-075 (IMI-040cp)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION (617) 227-5941
INFORMATION CON SEQUENCE CHARACTERISTICS:
LENGTH: 20 mains acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 56;
                           E: LAHIVE & COCKFIELD
60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/440,861
FILING DATE: 15-MAY-1995
FLISSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-440-861-14; Sequence 14, Application US/08440861
Patent No. 5710126; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 20.2%;
Best Local Similarity 55.0%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATPEAKYDAFVTALTEALRV 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 AAPEDKYEAFVLHFSEALHI 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide
internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 60 State Stre
CITY: Boston
STATE: Massachusetts
CORRESPONDENCE ADDRESS:
                                                                                                                    Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOLECULE TYPE:
FRAGMENT TYPE:
US-08-440-861-13
                                                                                        Boston
                                                                                                                                                                        02109
                                                                                                                 STATE: Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                Sequence 11 Application US/08440861

Patent No. 5710126

GENERAL INFORMATION:

APPLICANT: Griffith, Irwin J.

APPLICANT: Ludgman, Mohammad

APPLICANT: Ludgman, Mohammad

APPLICANT: Ludgman, Mohammad

APPLICANT: Ludgman, Mohammad

TITLE OF INVENTION: ALLERGEN

TITLE OF INVENTION: ALLERGEN

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, suite 510

CITY: Boston

STREET: Boston

ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 57; DB 1; Length 20;
Pred. No. 0.22;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13, Application US/08440861
Patent No. 5710126
GENERAL INFORMATION:
APPLICANT: Griffith, Irwin J.
APPLICANT: Lugman, Mohammad
TITLE OF INVENTION: T CELL EPITOPES OF RYEGRASS POLLEN
TITLE OF INVENTION: ALLERGEN
NUMBER OF SEQUENCES: 56
                                                       |: || ||: | ||:||
| YDVAYKAAEGATPEAKYDAF 20
                     10 YNAAYNAADHAAPEDKYEAF 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.6%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |:|||| |: || ||: || 3 LIPKLDTAYDVAYKAAE 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LVPKLDEVYNAAYNAAD 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-440-861-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                             US-08-440-861-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-440-861-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
```

В

ò

ö

Gaps

; 0

```
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-433-854-28
                                                                                                                                                                                              40 IAGTPEVHAVKP 51
                                                                                                                                                                                                                        |||| |||||||
|1 IAGALEVHAVKP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 IAGTPEVHAVKP 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-174-745A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5721119ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                      19.5%; Score 54; DB 1; Length 20; 60.0%; Pred. No. 0.56; tive 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,854
FILING DATE:
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,060
FILING DATE: 14-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                       NAME: Amy Bandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 1PC-075 (IMI-040cp)
TELECOMMUNICATION INFORMATION:
TELEFRONE: (617) 227-7400
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Singh, Mohan Bir
APPLICANT: Singh, Mohan Bir
APPLICANT: Smith, Penelope
APPLICANT: Smith, Penelope
APPLICANT: Theerakulpisut, Asil
APPLICANT: Hough, Terryn
APPLICANT: Hough, Terryn
APPLICANT: Ong, Eng Kok
APPLICANT: Ong, Eng Kok
APPLICANT: Ong, Eng Kok
APPLICANT: Suphioglu, Cenk
APPLICANT: Ong, Eng Kok
APPLICANT: Ong, Eng Kok
CORRESPONDENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/POCKET NUMBER: IMPH-0024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-349
INFORMATION FOR SEQ ID NO: 28:
APPLICATION NUMBER: US 08/106,016 FILING DATE: 31-AUG-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 28, Application US/08433854
Patent No. 5721119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 VLHFSEALHIIAGTPEVHAV 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 19.39
Best Local Similarity 60.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 13 amino acids amino acids
                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U. ZIP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-433-854-28
                                                                                                                                                                                                                                                                                                                                          US-08-440-861-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ong, Eng Kok
TTLE OF INVENTION: Ryegrass Pollen Allergen
NUMBER OF ENUENTION: Ryegrass Pollen Allergen
NUMBER OF SEQUENCES: S
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5736362ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
    Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/174,745A
      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 48; DB 1;
Pred. No. 2.1;
0; Mismatches
    Score 48; DB :
Pred. No. 2.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: IMPH-0024
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,060
FILING DATE: 14-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                    US-08-174-745A-28; Sequence 28, Application US/08174745A; Patent No. 5736362
                                                                                                                                                                                                                                                                                                                                                                       Theerakulpisut, Piyada
  17.3%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 28
                                                                                                                                                                                                                                                                                  APPLICANT: Singh, Mohan Bir
APPLICANT: Knox, Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.3%;
83.3%;
                                                                                                                                                                                                                                                                                                                                Smith, Penelope
Avjioglu, Asil
                                                                                                                                                                                                                                                                                                                                                                                        Hough, Terryn
Suphioglu, Cenk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 13 amino acids
amino acid
Query Match 17.3
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 19103
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
```

```
17.3%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 17.3
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: peptide US-08-433-885-28
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 IAGTPEVHAVKP 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                   COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U
                                                                                                    ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-433-908B-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Macklewicz & No. 5840316ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.3%; Score 48; DB 2; Length 13; 83.3%; Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/195,947
FILING DATE: 14-FEB-1994
CLASSIFICATION NUMBER: US 07/930,060
FILING DATE: 14-AGG-1992
ATTORNEY/AGENT INFORMATION:
NAME: HODENSCHUEZ, LIZa D.
RECISTRATION NUMBER: MARCHESTRATION SEG 1515 568-3100
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3100
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hough, Terryn
APPLICANT: Suphioglu, Cenk
APPLICANT: Ong, Eng Kok
TITLE OF INVENTION: Ryegrass Pollen Allergen
                                                                                                                                                      APPLICANT: Avjioglu, Asil
APPLICANT: Theerakulpisut, Piyada
APPLICANT: Hough, Terryn
APPLICANT: Suphioglu, Cenk
APPLICANT: Suphioglu, Cenk
APPLICANT: ONG, Eng Kok
APPLICE OF INVENTION: Ryegrass Pollen Allergen
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 28, Application US/08433885
Patent No. 586933
GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir
APPLICANT: Smith, Penelope
APPLICANT: Smith, Penelope
APPLICANT: Theerakulpisut, Piyada
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                               Sequence 28, Application US/08195947
Patent No. 5840316
GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir
APPLICANT: Knox, Robert B.
APPLICANT: Smith, Penelope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 17.3
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19103
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 IAGTPEVHAVKP 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||| |||||||
| IAGALEVHAVKP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-195-947-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-433-885-28
                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
```

```
CONTENT OF STATES OF STATE
```

ö

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                             DB 4; Length 13;
                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.3%; Score 48; DB 1; Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                Sequence 15, Application US/08440861
Patent No. 5710126
GENERAL INFORMATION:
APPLICANT: Kuo, Mei-Chang
APPLICANT: Luqman, Mohammad
TITLE OF INVENTION: T CELL EPITOPES OF RYEGRASS POLLEN
TITLE OF INVENTION: ALLERGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,861
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/106,016
FILING DATE: 31-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: AMP. E. MANDARGAGOURAS
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
TELECOMMUNICATION: INFORMATION:
TELECOMMUNICATION: INFORMATION:
                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                            Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-08-214-770-8
Sequence 8, Application US/08214770
; Patent No. 5523209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 17.3
Best Local Similarity 83.3
Matches 10; Conservative
                                                                            Query Match 17.3
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide
internal
   peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Massachusetts
                                                                                                                                                        40 IAGTPEVHAVKP 51
                                                                                                                                                                           1 IAGALEVHAVKP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 40 IAGTPEVHAVKP 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IAGALEVHAVKP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOLECULE TYPE:
FRAGMENT TYPE:
US-08-440-861-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boston
   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
     ;
US-08-410-614-28
                                                                                                                                                                                                                                                 RESULT 11
US-08-440-861-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q
                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 6277383ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                             ·,
                                                                                                                                                                                                                                                                                                        Length 13;
                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hough, Terryn
APPLICANT: Suphisoglu, Cenk
APPLICANT: Ong, Eng Kok
TITLE OF INVENTION: Ryegrass Pollen Allergen
                                                                                                                                                                                                                                                                                                                                           0; Mismatches
               NAME: Mandragouras, Any E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-039C2D4
TELECOMMUNICATION INFORMATION:
TELEFAN: (617) 227-7400
TELEFAN: (617) 742-4214
INFORMATION FOR SEQ. ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/195,947
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 07/930,060
FILING DATE: 14-AUG-1992
ATTORNEZ/AGENT INFORMATION:
NAME: HOHENSCHULZ, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/POCKET NUMBER: IMPH-0024
                                                                                                                                                                                                                                                                                                        Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Singh, Mohan Bir
Knox, Robert B.
Smith, Penelope
Avjioglu, Asil
Theerakulpisut, Piyada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-08-410-614-28
; Sequence 28, Application US/08410614
; Patent No. 6277383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                    17.3%;
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                       Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 13 amino acids TYPE: amino acid
                                                                                                                                                                                                      TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-433-908B-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                    40 IAGTPEVHAVKP 51
                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                      Query Match
```

ò

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5; Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Griffith, Irwin J.
APPLICANT: Kuo, Mei-Chang
APPLICANT: Kuo, Mei-Chang
APPLICANT: Luqman, Mohammad
TITLE OF INVENTION: T CELL EPITOPES OF RYEGRASS.POLLEN
TITLE OF INVENTION: ALLERGEN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFRENCE/DOCKET NUMBER: IPC-075 (IMI-040cp)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUIDNE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43.5; i
Pred. No. 29;
                                                                                                                                                                                                       06410/002001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRK: USA
2IP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,861
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION 1435
PRIOR APPLICATION NUMBER: US 08/106,016
FILING DATE: 31-AUG-1993
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                     APPLICATION NUMBER: PCT/US95/02885
                               FILING DATE:
CLASSIETCATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/214,770
FILING DATE: March 14, 1994
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKEY NUMBER: 06410/00
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 542-8906
TELEFEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/08440861
Patent No. 5710126
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.7%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 YNAAYNAAD-HAAPEDK 25
  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY:
PCT-US95-02885-8
                                                                                                                                                                                                                                                                                                                                                     LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-440-861-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application PC/TUS9502885
GENERAL INFORMATION:
APPLICANT: Ginsberg, Mark H.
APPLICANT: O'TOOLe, Timothy
TITLE OF INVENTION: METHODS FOR IDENTIFYING INHIBITORS
TITLE OF INVENTION: OF INTEGRIN ACTIVATION
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                APPLICANT: Ginsberg, Mark H.
APPLICANT: O'TOOLe, Tim
TITLE OF INVENTION: METHODS FOR IDENTIFYING
TITLE OF INVENTION: INHIBITORS OF INTEGRIN
TITLE OF INVENTION: ACTIVATION
ACTIVATION
CORRESPONDENCE: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STAIL.

COUNTRY: U.S.A.
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: WordPerfect (Version 5.1)
                                                                                                                                                                                                                 COUNTRY: U.S.A.

ZIP: 02110-2804
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: TBM PS/2 Model 502 or 558X
OPERATING SYSTEM: MS-DOS (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/214,770
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 43.5;
Pred. No. 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 06410/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Fish & Richardson 225 Franklin Street
                                                                                                                                                            ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.7%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 YNAAYNAAD-HAAPEDK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1:| |: |: || || 1|
13 YDATYHKAEIHAQPSDK 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 9; Conserv
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 225 F
                                                                                                                                                                                 STREET: 225 F
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
PCT-US95-02885-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-214-770-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

÷

```
qq
                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPARE: PatentIn Release #1.0, Version #1.25 (EPO)
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CUASSIFICATION DATA:
APPLICATION NUMBER: US/08/900,574
FILING DATE: July 24, 1997
CLASSIFICATION NUMBER: German Application No. 6221837 19630242.0
FILING DATE: July 26, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Carcl P: Einaudi
RESISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 02481.1499-00000
TELECOMMUNICATION INFORMATION:
METERINGE TO THE PROPRIATION:
METERING TO THE PROPRIATION TO THE PROP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08900574
Patent No. 6221837
GENERAL INFORMATION
APPLICANT: Ertl, Johann
APPLICANT: Geisen, Karl
APPLICANT: Seine, Karl
APPLICANT: Seine, Gerhard
TITLE OF INVENTION: Insulin derivatives with increased zinc
TITLE OF INVENTION: binding
NUMBER OF SEQUENCE: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 44.48; Pred. No. 30;
Matches 8; Conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.4%; Score 40; DB 4; Length 53; 36.4%; Pred. No. 1.4e+02; tive 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Finnegan, Henderson, Farabow, Garrett,
ADDRESSEE: 6 Dunner, L.L.P.
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREE: 1300 - CTTY: Washington STATE: District of Columbia COUNTRY: U.S.A. 7TP: 20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Escherichia coli FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPANE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 4:
SEGUENCE CHARACTERISTICS:
LENGTH: 53 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :| | ||: | |||:
1 NAPPADKFKIFEAAFSES 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 HAAPEDKYEAFVLHFSEA 36
TYPE: amino acid

TOPOLOGY: 'linear

MOLECULE TYPE: peptide

; FRAGMENT TYPE: internal

US-08-440-861-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: Amino acid
STRANDEDNESS: Single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: Protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION:
US-08-900-574-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-08-900-574-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                         õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
```

```
July 11, 2002, 11:03:13 ; Search time 18.29 Seconds (without alignments) 299.458 Million cell updates/sec
GenCore version 4.5
|Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                 - protein search, using sw model
                                                                                              OM protein
                                                                                                                                             Run on:
```

US-09-696-169A-21 275 1 MARHKFWVAMFLAVAVVLGL......LIEDVNASFRAAMATTANVP Title: Perfect score: Sequence:

57

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

Total number of hits satisfying chosen parameters: 283138 segs, 96089334 residues Searched:

14670

Minimum

DB seq length: 0 DB seq length: 57 Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries pirl:\* pir2:\* pir3:\* pir4:\* PIR\_71:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is deriyed by analysis of the total score distribution.

	Description	pollen allergen DG	osomal pr	•	endoglucanase B (E	photosystem I prot			immune-inducible p	hypothetical prote	hypothetical prote	probable secreted	tms1 protein - mou	nikkomycin synthes	ribosomal protein	8	probable NADPHfe	hydrogen dehydroge		tyrosine 3-monooxy	tyrosine 3-monooxy	tyrosine 3-monooxy	tyrosine 3-monooxy	ribosomal protein	hypothetical prote	·	dehyd	photosystem II pro	R2R3-MYB transcrip	gene 4f-rnp protei
SUMMARIES	QI	A60359	AC3544	B45246	A45959	T07505	H75292	T20751	S63981	S03775	AI1895	G87230	S54144	S61280	F87344	A28911	T06541	S03945	PN0589	PN0590	PN0591	PN0592	PN0593	JQ0732	C71316	LBBCB	D37334	· S10315	T52279	869595
	DB		7																											
	Length	28	44	51	52	30	49	48	52	47	26	57	44	38	44	52	20	33	45	45	45	45	45	47	49	20	55	39	45	33
	& Query Match	9.1	9	'n.	4.9	4	4.	4.5	₹.	4.4	₹.	4	4	3.8	ω.	ω,	Э.	ω.	ω.	ω.		•		•		•			•	
•	ν α Wa	7	1	7	H	_	H	٦	7	-	H	٦	Ä	П	_	-	П		-	-	-		H	-	7	H	H	H	H	-
	Score	80	45	41.5	-		40.5	40	4	٥.		m	38.5	38	38	c	37.5	37	37	37	37	37	37	37	37		'n	36.5	9	36
	Result No.	-	2	٣	4	2	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

8 2 S76107 8 2 C83437 0 2 D90706 3 2 B4236 4 1 BGSH 5 2 E83079 7 2 A42906 7 2 A50109 5 2 T52125 7 2 G87679 7 2 E87394 8 2 S33918	 00000000000000000	photosystem II pro	photosystem in pro	hypothetical prote		hypothetical prote	spermatid transiti	hypothetical prote	hypothetical prote	conserved hypothet	dnaK-type molecula	hypothetical prote	RZR3-MYB transcrip	hypothetical prote	hypothetical prote	myrosinase - chick
88800EE470674427714 24476744444444444444444444444444444444	133.1. 133.1. 133.1. 122.7. 122.7. 122.7. 122.7.	S76107	C83437	D90706	H84193	B84236	BGSH	A70070	E83079	AH2906	S32408	A95019	T52125	G87679	E97394	S31918
	133.1. 133.1. 133.1. 122.7. 122.7. 122.7. 122.7.	2 2	4 0	0 0	3 2	3	4	2	2	7 2	4 2	2	2	7 2	1 2	4

## ALIGNMENTS

```
CiSpecies: Dactylis glomerata (orchard grass)
CiSpecies: Dactylis glomerata (orchard grass)
CiSpecies: Dactylis glomerata (orchard grass)
CiSpecies: O3-Reb-1993 #sequence_revision 03-Feb-1993 #text_change 03-Nov-2000
CiAccession: A60359
R;Walsh, D.J.; Matthews, J.A.; Denmeade, R.; Maxwell, P.; Davidson, M.; Walker, M.R. Int. Arch. Allergy Appl. Immunol. 91, 419-425, 1990
A;Title: Monoclonal antibodies to proteins from cocksfoot grass (Dactylis glomerata)
A;Reference number: A60359; MUID:91007970
A;Residues: 1-28 GWAL>
C;Superfamily: grass pollen allergen IX
C;Keywords: pollen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 80; DB 2; Length 28;
Pred. No. 0.0046;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 29.1%;
Best Local Similarity 75.0%;
Matches 15; Conservative
```

26 AEGGKATTEEQKLIEDVNAS 45 9 AAGGKATTEEQKLMEDINXA 28 RESULT ŏ QQ

LSU ribosomal protein 134P [imported] - Brucella melitensis (strain 16M)
C; Species: Brucella melitensis
C; Species: Brucella melitensis
C; Species: Orber 2002 #sequence\_revision 01-Feb-2002 #text\_change 01-Feb-2002
C; Accession: AC354W
R; DelVacchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov, Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A; Title: The genome sequence of the facultative intracellular pathogen Brucella melit A; Reference number: A03522; PMID:11756688 A;Molecule type: DNA A;Residues: 1.44 <KUR> A;Cross-references: GB:AE008918; PIDN:AAL53518.1; PID:g17984424; GSPDB:GN00191 Score 45; DB 2; Length 44; Pred. No. 1.2e+02; 3; Mismatches 11; Indels A; Experimental source: strain 16M 16.48; 41.78; Query Match 16.4 Best Local Similarity 41.7 Matches 10; Conservative A; Status: preliminary A; Map position: II C;Genetics: A;Gene: BMEI0276

ö

Gaps

; 0

```
A;Cross-references: GB:AE002060; GB:AE000513; NID:g6460082; PIDN:AAF11832.1; PID:g646
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR2276
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: H75292
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R. M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C. S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rigardner, A. submitted to the EMBL Data Library, March 1997
A; Reference number: 219319
A; Reference number: 219319
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-48 < MIL.
A; Cross-references: EMBL: 292830; PIDN: CAB07358.1; GSPDB: GN00023; CESP:F11A5.6
A; Experimental source: clone F11A5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec_1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F11A5.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20751
                                                                                                                                             A;Cross-references: EMBL:D17510; NID:9529643; PIDN:BAA04316.1; PID:91262597
C;Genetics:
   A; Cross-references: EMBL: D17510; NID: 9529643; PIDN: BAA04316.1; PID: 91262597
                                                                                                                                                                                                           A;Gene: psam
A;Genome: chloroplast
C;Keywords: chloroplast; photosynthesis; photosystem I; thylakoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 49;
                                                                                                                                                                                                                                                                                                                                                              Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                        Query Match 14.7%; Score 40.5; DB 2; Best Local Similarity 42.3%; Pred. No. 2.8e+02; Matches 11; Conservative 4; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40.5; DB 2;
Pred. No. 4.7e+02;
3; Mismatches 3;
                     A; Accession: T07436
A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA
A; Residues: 1-30 < WA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAAHKFMVAMFLA----VAVVLGLA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.7%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 MFLAVAVVLGLATSPTA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :|| ||:| |: | |||
16 IFLVVALVWGM-TGPTA 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: H75292
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-49 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Genetics:
A;Gene: CESP:F11A5.6
A;Map position: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cispecies: Cellulomonas fimi
C;Species: Cellulomonas fimi
S;Owolabi, J.B.; Beguin, P.; Kilburn, D.G.; Miller Jr., R.C.; Warren, R.A.J.
Appl. Environ. Microbiol. 54, 518-523, 1988
A;Title: Expression in Escherichia coli of the Cellulomonas fimi structural gene for end
A;Reference number: A45959
A;Accession: A45959
A;Actus: preliminary
A;Molecule type: DNA
A;Status: 1-55 cowo>
A;Cross-references: GB:M33026; NID:g144413; PIDN:AAA23085.1; PID:g144414
A;Note: the authors translated the codon CAC for residue 53 as Gln, and TCC for residue
C;Keywords: g1ycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: chloroplast Pinus thunbergiana pine cultotypiast.
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 18-Aug-2000
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 18-Aug-2000
C;Accession: T07505; T07436
R;Wassugi, T; Tsudzuki, J; Ito, S; Nakashima, K; Tsudzuki, T.; Sugiura, M. Proc. Natl. Acad. Sci. U.S.A. 91, 9794-9798, 1994
A;Title: Loss of all ndh genes as determined by sequencing the entire chloroplast genome A;Reference number: 216030; MUID:95024047
                                                                                                                                                                                                                                C; Species: Lactococcus lactis subsp. lactis

C; Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994

C; Accession. B45246

R; Llanos, R.M.; Hillier, A.J.; Davidson, B.E.

J; Bacteriol. 174, 6956-6964, 1992

A; Title: Cloning, nucleotide sequence, expression, and chromosomal location of 1dh, the

A; Reference number: A45246; MUID:93015759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid A;Molecule type: nucleic acid A;Residues: 1-51 <LLA> A;Residues: 1-51 <LLA> A;Note: sequence extracted from NCBI backbone (NCBIP:116909)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.9%; Score 41; DB 2; Length 55;
40.0%; Pred. No. 4.6e+02;
tive 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      photosystem I protein psam - Japanese black pine chloroplast
                                                                                                                                                                                                           orf 3'of 1dh - Lactococcus lactis subsp. lactis (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41.5; DB 2;
Pred. No. 3.7e+02;
7; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule types DNA
A;Residues: 1-30 (4)AK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAAHKFMVAMFLAVAVVLGLATSPTAEG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 MAPYVFTI---IVLALFLGKAIAPKADG 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 MVAMFLAVAVVLGLATSPTAEGGKA 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23
                                    2 KRTYQPSKIVRKRRHGFRARMATT 25
30 KATTEEQKLIEDVNASFRAAMATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.1%;
ilarity 35.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 40.0°
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A45959
ò
                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

٦. ٢.

Ĥ

Gaps

5

;

Gaps

ü

```
14.4%;
32.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 14.2%;
Best Local Similarity 29.4%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-44 < KUS>
A; Cross-references: EMBL: X86374
                                                                                                                                                                                                                                                                                                                                                        Query Match 14.4
Best Local Similarity 32.1
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: S54144
A; Accession: S54144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: ML2569A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
S54144
                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                    Januarie-Inducible proline-rich protein precursor - fruit fly (Drosophila melanogaster)

N.Alternate names: metchnikowin
C.Species: Drosophila melanogaster
C; Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
C; Accession: S63981; S63980
C; Accession: S63981; S63980; Multesser, S.; Bulet, P.; Reichhart, J.M.; Hetru, C.; Hoffmann, J.A.
Eur. J. Biochem. 233, 694-700, 1995
A; Title: Metchnikowin, a novel immune-inducible proline-rich peptide from Drosophila wit
A; Reference number: S63980; MUID:96067716
A; Accession: S63980; MUID:96067716
A; Accession: S63980
A; Molecule type: mRNA
A; Residues: 1-52 <LEV>
A; Cross-references: GB:X91060; NID:91052588; PIDN:CAA62511.1; PID:91052589
A; Note: 19-Th., 29-Arg was also found
A; Molecule type: protein
A; Residues: 27-52 <LEW>
A; Molecule type: protein
A; Residues: 27-52 <LEW>
A; Note: 3-Arg was_also found
A; Note: 3-Arg was_also found
B; 1-26/Domain: signal sequence #status predicted <SIG>
F; 27-52/Product: immune-inducible proline-rich protein #status predicted <MAT>
Exp. 27-52/Product: immune-inducible proline-rich protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI1895
hypothetical protein as10715 [imported] - Anabaena sp. (strain PCC 7120)
C;Species: Anabaena sp.
A;Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
                                             3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 47;
  Length 48;
Score 40; DB 2; Length 48;
Pred. No. 5.3e+02;
6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 FLAVAVVLGLATSPTAEGGKATTEEQKLIEDVNASFRAAMATTA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39.5; DB 2;
Pred. No. 5.9e+02;
5; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40; DB 2;
Pred. No. 5.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                 17 VLGLATSPTAEGGK-ATTEEQ--KLIE 40
                                                                                                         :|| | ||:|:| | ||:|
23 ILGFA-SPSAQGTESASTRSQGAKLVE 48
14.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.5%;
52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 14.4%;
Best Local Similarity 34.1%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 AIFLALLGYMATATSVLAE 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 AMFLAVAVVLGLATSPTAE 27
                                        13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 10; Conserve
                       Best Local Similarity
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QQ
                                                                                   õ
                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

```
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUD:21595285; PMID:11759840
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-56 <KURN>
A;Residues: 1-56 <KURN>
A;Cross-references: GB:BA000019; PIDN:BAB72672.1; PID:g17130060; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: as10715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-57 <STO>
A;Cross-references: GB:AL450380; NID:g13093813; PIDN:CAC32101.1; GSPDB:GN00147
C;Genetics:
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan;2002 C;Accession: A11895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tms1 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jul-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 FGFALMLSLAAFLGACGETQTPPPAATGEPT-----DTGAATPAATP 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 FMVAMFLAVAVVLGLA----TSPTAEGGKATTEEQKLIEDVNASFRAAMATTANVP
                                                                                                                                                                                                                                                                                                                                                                                                                          Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable secreted protein [imported] - Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39.5; DB 2;
Pred. No. 7.1e+02;
5; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39; DB 2; Pred. No. 8.3e+02; 4; Mismatches 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | | : | : | | : | 8 AAASVVVGLLLGAATIFGMTLMVQQDTKPPLPGG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AAHKFMVAMFLAVAVVLGLA----TSPTAEGG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: 554144
R;Kustikova, O.S.
submitted to the EMBL Data Library, April 1995
```

```
Search completed: July 11, 2002, 11:05:21 Job time: 128 sec
            A; Reference number: A28911; MUID:88282537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nikkomycin synthesis protein P6 - Streptomyces tendae (fragments)
(5.Species: Streptomyces tendae
(5.Species: Streptomyces tendae
(5.Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
(5.Accession: 561280
(7.May-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
(7.May-1996 #sequence 0.; Bormann, C.
(7.May-1996 #sequence 0.; Bormann, C.
(7.May-1996 #sequence 0.; Bormann, C.
(7.May-1999 #sequence 0.; Bormann, C.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cipecies: Caulobacter crescentus
Cipecies: Caulobacter crescentus
Cipecies: Caulobacter crescentus
Cipecession: F89344
R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Status: Preliminary
A;Status: Preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAlternate names: paragonial peptide
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Accession: A28911
R;Chen, P.S.; Stumm-Zollinger, E.; Aigaki, T.; Balmer, J.; Bienz, M.; Boehlen, P.
Cell 54, 291-299, 1988
A;Title: A male accessory gland peptide that regulates reproductive behavior of female I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-44 <STO>
A; Cross-references: GB:AE005673; NID:g13422006; PIDN:AAK22754.1; GSPDB:GN00148
C; Genetics:
A; Gene: CC0769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - fruit fly (Drosophila melanogaster)
                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                              5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
            Length 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38; DB 2; Length 30;
Pred. No. 7.2e+02;
Control of the prediction of the predi
                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB 2; Length 44;
Pred. No. 8.4e+02;
3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ribosomal protein L34 [imported] - Caulobacter crescentus
Score 38.5; DB 2;
Pred. No. 7.3e+02;
2; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   male accessory gland peptide precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 KATTEEQKLIEDVNASFRAAMAT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 AVAVVLGLATS----PTAEGG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.8%;
39.1%;
14.0%;
45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.8%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 13.89
Best Local Similarity 39.19
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 13.8
Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 LATSPTAEGGKATTEE 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||| ||| ||: | |:
22 LATMPTADVAKIAVED 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: 1-20;21-38 <MOE>
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

```
A, Accession: A28911
A, Molecule type: mRNA
A, Residues: 1-55 cHB>
A, Cross-references: GB:M21201; NID:g158124; PID:g158125
A, Cross-references: GB:M21201; NID:g158124; PID:g158125
A, Note: part of this sequence, including the amino end of the mature protein, was det C, Genetics:
A, Genetics: A, Genetics: FlyBase:Acp70A
A, Cross-references: FlyBase:FBgn0003034
C, Keywords: hydroxyproline
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-55/Product: male accessory gland peptide #status experimental <MAT>
F:20-55/Productine derivative (Ile) #status experimental
F:33/Modified site: isoleucine derivative (Ile) #status experimental
F:33-FD:M0dified bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 2; Length 50;
Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.8%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 13.8
Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 VAMFLAVAVVLGLATS 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 LALFLVLVCVLGLVQS 19
```

ć

ĕ

```
Phycoerythrin
Chroomonas sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
                                                                          July 11, 2002, 11:04:58; Search time 10.15 Seconds (without alignments) 217.440 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P30942 chroomonas
P4071 bacillus su
C24435 drosophila
Q9cd20 mycobacteri
P5812 caulobacter
P5623 drosophila
P22659 rhodococcus
C2592 photobacter
P2636 proteus mir
P26274 erythrobact
C8536 treponema p
P58340 mycobacteri
P58340 mycobacteri
P7747 synechococc
C5467 synechococc
C5766 methanococc
C67966 methanococc
C67967 methanococc
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ovis aries
cucurbita m
bacillus an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P41601 pinus thunb
                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                           57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                             US-09-696-169A-21
275
1 MAHKFWVAMFLAVAVVLGL......LIEDVNASFRAAMATTANVP
                                                                                                                                                                                                                                                     4574
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                          105224 seqs, 38719550 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VG38_BPMD2
Y474_BORBU
RL34_CHLMU
                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                   - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rc21_arcfu
                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                      SwissProt_40:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    length: 0
length: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
Perfect score:
                                                                                                                                                                                                                                                                            Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                   Scoring table:
                                                   protein
                                                                                                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                        Sequence:
                                                                                                                                                                                                                           Searched:
                                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Result
```

34 32 11.6 44 13 35 35 35 35 35 32 11.6 44 13 37 32 11.6 45 13 39 32 11.6 46 13 39 32 11.6 50 14 40 32 11.6 50 14 42 32 11.6 52 14 42 32 11.6 52 11.6	P45647 coxiella bu P3349 mycoplasma Q92cu9 rickettsia Q84790 chlamydia t P0247 escherichia P4244 haemophilus P16548 drosophila P17306 sus scrofa O1866 drosophila Q06173 desulfovibr P09641 myoxocephal P35097 rhodopseudo	AA.  ite)  (PSI-M).  ack pine).  abryophyta; Tracheophyta;  Pinaceae; Pinus.  na K., Tsudzuki T.,	duced through a collaboration s and the EMBL outstation are no restrictions on its its content is in no way Usage by and for commercial tp://www.isb-sib.ch/announce/	1; Length 30; 2; 6; Indels 5; Gaps 1;
and	4 4 4 4 4 4 6 7 6 7 7 8 4 4 4 4 4 7 7 7 7 7 8 7 7 8 7 8 7	ALIGNMENTS  STANDARD; PRT; 30 AA.  (Rel. 32, Last sequence update) (Rel. 34, Last annotation update) I reaction centre subunit XII (PSI-M).  rgii (Green pine) (Japanese black pine). iridiplantae; Streptophyta; Embryophyta; a; Coniferopsida; Coniferales; Pinaceae; 350;  M N.A.  4047; PubMed=7937893; Tsudzuki J., Ito S., Nakashima K., Tsud ndh qenes as determined by sequencing t	genome of the black pine Pinus thunberging Acad. Sci. U.S.A. 91:9794-9798(1994).  TY: BELONGS TO THE PSAM FAMILY.  ROT entry is copyright. It is produced to swiss Institute of Bioinformatics and Bloinformatics and Bloinformatics and Bloinformatics and Institutions as long as its corp. This statement is not removed. Usage this statement is not removed. Usage units a license agreement (See http://www.mail. to license@isb-sib.ch).  BAA04383.1;  BAA04383.1;  BAA04316.1;  I; Photosynthesis; Chloroplast.  O AA; 3321 MW; Al50441AB5D5AF7C CRC64;	larity 42.3%; Score 40.5; DB 1; larity 42.3%; Pred. No. 1.3e+02; Conservative 4; Mismatches 6 VAMFLAVAVVLGLA 21 :
200 000 000 000 000 000 000 000 000 000	31	PINTH PSAM_PINTH P41601; PONV-1995 01-NOV-1995 01-OCT-1996 Photosystem PSAM_PINTH PAGAS 01-NOV-1995 01-OCT-1996 PROCENTY PSAM_PINTH PSAM_PINTH PSAM_PINTH PSAM_PINTH NCBL_TAIND=-3502 WARASUGIT T. SUGILNE=9502 WARASUGIT T.	chloroplast Proc. Natl	ry Ma t Loc ches 1 1 1 2 CHRSP PHEL P3094 01-JU 01-JU 01-JU
######################################		[D8]	8 % B B C C C C C C C C C C B B B C C C C	According Date of Date

```
Matches
                                                                                                                                                                                                 MTK_DROME
                                                                                                                                                                              RESULT
                                                                                                                          g
                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                      -1- SUBCELLULAR LOCATION: WITHIN THE THYLAKOID LUMEN. PERIPHERY OF THE RADOS OF THE PHYCOBLISOME.
-1- PTM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.
InterPro: IPRO04228; phycoerythr_ab.
                                                                                                                                                                                                                                                                   THE ALPHA SUBUNITS. THE 2(ALPHA/BETA) STRUCTURE COULD COMPRISE ANY COMBINATION OF 2 OUT OF 4 DIFFERENT ALPHA UNITS WITH AN INVARIANT
                                                                                                                                                                                       FEBS Lett. 273:191-194(1990).
-1- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN
FROM THE PHYCOBILIPROTEIN COMPLEX.
-1- SUBUNIT: THE ORIGIN OF MULTIPLE FORMS OF PHYCOBRYTHRIN MAY LIE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-89108019; PubMed-3145906;
Smith H., de Jong A., Bron S., Venema G.;
"Characterization of signal-sequence-coding regions selected from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                      Jenkins J., Hiller R.G., Speirs J., Godovac-Zimmermann J.; "A genomic clone encoding a cryptophyte phycoerythrin alpha-subunit. Evidence for three alpha-subunits and an N-terminal membrane transit
                                                                                                                                                                                                                                                                                                                                                                                                               Phycobilisome; Electron transport; Photosynthesis; Bile pigment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.7%; Score 40.5; DB 1; Length 44; 34.8%; Pred. No. 2e+02; Live 8; Mismatches 6; Indels
Eukaryota; Cryptophyta; Cryptomonadaceae; Chroomonas.
NCBI_TaxID=3029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4696 MW; 548FA6DF26755CA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 44 AA; 4723 MW; 2EBE2D2EAF47AA7E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein clone PSP28 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SubtiList, BG11031; yzqA.
Hypothetical protein; Complete proteome.
                                                                                                      MEDLINE-91032178; PubMed-2226853;
                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02972; phycoerythr_ab;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 GLATSPTAE-GGKATTEEQKLIE 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | : :| :| || || ::| :::
GCSRAPKSETGGTATKDDQMMVK 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus subtilis chromosome.";
Gene 70:351-361(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M22915; AAA22831.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    44
                                                                                                                                                                                                                                                                                                     BETA UNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                   Chloroplast.
                                                                                                                                                                            sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YZQA_BACSU
P40771:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YZQA_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18
                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         õ
```

```
RECENTERE FROM N.A.

RECENTER FROM N.
                                                  ï
                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Levashina E.A., Ohresser S., Lemaitre B., Imler J.-L.; myo distinct pathways can control expression of the gene encoding the Drosophila antimicrobial peptide metchnikowin."; J. Mol. Biol. 278:515-527(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Metchnikowin, a novel immune-inducible proline-rich peptide from Drosophila with antibacterial and antifungal properties."; Eur. J. Biochem. 233:694-700(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-96067716; PubMed-7588819;
Leyashina E.A., Ohresser S., Bulet B., Reichhart J.-M., Hetru C.,
                                                  3;
     DB 1; Length 44;
                                                    Indels
  Score 40.5; DB 3 Pred. No. 2e+02;
                                                                                                                                                                                                                                                               MTK_DROME STANDARD; PRT; 52 AA. 024395; 024396; 09V7B9; 01-NOV-1997 (Rel. 35, Created) NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Metchnikowin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=OREGON-R; TISSUE=Abdomen, and Thorax;
                                                  5; Mismatches
                                                                                                 5 KFMVAMFLAVAVVLGLATSPT---AEGGKATTE 34
                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 27-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98263241; PubMed-9600835;
14.78;
39.48;
                                                    13; Conservative
       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-OREGON-R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hoffmann J.A.:
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodage T., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
The genome 'sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: HIGHEST EXPRESSION IN FAT BODY. MAYBE BLOOD CELLS PARTICIPATE IN THE PRODUCTION OF THE PEPTIDE.
DEVELOPMENTAL STAGE: EXPRESSED RAPIDLY AND STRONGLY AT ALL STAGES. POLYMORPHISM: 2 ALLELIC FORMS (A1 AND A2) VARYING IN TWO AA SOSTION. THE ISOFORM SHOWN HERE IS A1.
SIMILARITY: TO DIPTERICIN, HEMIPTERICIN, DROSOCIN, APIDABCINS AND TO THE C-TERMINUS OF ABARCIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBL_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: POTENT ANTIFUNGAL AND ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 1; Length 52;
Pred. No. 2.7e+02;
Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A -> T (IN STRAIN A2).
H -> R (IN STRAIN A2).
OBIE2112BAE03129 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YESOUR STANDARD; PRT; 57 AA. 1738_MYCLE STANDARD; PRT; 57 AA. 202020; DT 16-0CT-2001 (Rel. 40, Last sequence update) DT 17, Dames R. Mbeller Erom N.A. Raylander T., Churcher C., RA Mungall K., Basham D., Brown D., Chillingworth T. RA Mungall K., Basham D., Brown D., Chillingworth T. RA Holroyd S., Honore N., Garnier T., Churcher C., RA Holroyd S., Honorey K., Dauthoy S., Feltwell T., FRA Holroyd S., Holrospy T., Jagels K., Lacroix C., Marchy L., Oliver K., Quail M.A., Rajandream M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insect immunity; Antibiotic; Fungicide; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METCHNIKOWIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF030959; AAC64659.1; -. EMBL; AE003811; AAF58139.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X91060; CAA62511.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAA62512.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.5%;
52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5654 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 AMFLAVAVVLGLATSPTAE 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 AIFLALLGVMATATSVLAE 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FlyBase; FBgn0014865; Mtk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 52.6
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26
19
29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25
27
19
29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X91061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROPEP
            RRANA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license@isb-sib.ch).

or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commercia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

STRAIN-ATCC 19089 / CB15;

STRAIN-ATCC 19089 / CB15;

MEDLINE-21173698; bubmed-11259647;

Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

Salzberg S.L., Venter J.C., Shappiro L., Fraser C.M.;

"Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                       PUTATIVE SECRETED PROTEIN ML2569.1.
7CC82EB212AC94C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proteobacteria; alpha subdivision; Caulobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                          Score 39; DB 1; Length 57;
Pred. No. 3.8e+02;
4; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                    Hypothetical protein; Signal; Complete proteome
                                                    "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rel. 40, Last asquence update)
Rel. 40, Last annotation update)
protein L34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00468; Ribosomal_L34; I.
PROSITE; PS00784; RIBOSOMAL_L34; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AAHKFMVAMFLAVAVVLGLA-----TSPTAEGG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 AAASVVVGLLLGAATIFGMTLMVQQDTKPPLPGG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44
                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ribosomal protein; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000271; Ribosomal_L34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                             EMBL; AL583926; CAC32101.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-00T-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequ
16-0CT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE005752; AAK22754.1; -.
                                                                                                                                                                                                                                                                                                                                                           57 AA; 5897 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                   29.48;
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 14.2
Best Local Similarity 29.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caulobacter crescentus.
                                                                                                                                                                                                                                                                                 Leproma; ML2569A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=69394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RPMH OR CC0769.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50S ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC0769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caulobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RL34_CAUCR
P58129;
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria;
                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
RL34_CAUCR
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

4

```
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOXU_RHOOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOXU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RA Admans M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkvan D., Bocchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkvan D., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Glodek D., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Borkov D., Ereraz C., Ferriar S., Fleischmann W.,
RA Glodek A., Goorg F., Gorrell J.H., Guz J., Gunn P., Harris N.L.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Tbegwam C.,
Ra Jalahi M., Kallsh F., Karlesh F., Karlesh F., Karlesh F., Karlesh F., Karlesh E., Kodira C.D., Kraft C., K
                                                                            ö
                                                                                                                                                                                                                   A70A_DROME STANDARD; PRT; 55 AA.
P05623; 0186629; 03V0745;
01-NOV-1988 (Rel. 09, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Accessory gland-specific peptide 70A precursor (Paragonial peptide B).
ACPT-0A OR PAPB OR CG17673.
                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A male accessory gland peptide that regulates reproductive behavior of female D. melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cirera S., Aguade M.N.;
Evolutionary history of the sex-peptide (Acp70A) gene region in
Drosophila melanogaster.";
Genetics 147:189-197(1997).
                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=OREGON-R;
MEDLINE=88282537; PubMed=3135120;
Chen P.S., Stumm-Zollinger E., Algaki T., Balmer J., Bienz M.,
                           Score 38; DB 1; Lengtn 4., Pred. No. 3.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-M2, M11, M26, M36, M40, M47, M54, M55, AND M66;
MEDLINE-97432799; PubMed-9286679;
587E687C6BE1107A CRC64;
                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 20-55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20196006; PubMed=10731132;
                                                                                                           30 KATTEEQKLIEDVNASFRAAMAT 52
                                                                                                                                       2 KRTFOPSKLVRARRHGYRARMAT 24
5194 MW;
                                             13.8%;
39.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of female D. melanogaster.
Cell 54:291-298(1988).
                                                                            Conservative
                             SEQUENCE FROM N.A. STRAIN=BERKELEY;
44 AA;
                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boehlen P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [2]
SEQUENCE 1
SEQUENCE
                                                                                                                                                                                                      A70A_DROME
                                                                                                                                                                                        RESULT
တ္တ
                                                                                                           ò
                                                                                                                                        g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier B., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Weiliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O., Zheng R.A., Myers E.W., Rubin G.M., Venter J.C.; The genome sequence of Drosophila melanogaster."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1991 (Rel. 19, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
NAD-reducing hydrogenase hoxS gamma subunit (EC 1.12.1.2) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: MAIN CELLS OF THE ACCESSORY GLANDS OF MALES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S -> A (IN STRAINS M2, M26, M36, M40, M55 AND BERKELEY).
F6827A1F025BF23D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSORY GLAND-SPECIFIC PEPTIDE 70A.
                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: REPRESSES FEMALE SEXUAL RECEPTIVITY AND STIMULATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHEMICAL NATURE NOT DETERMINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB 1; Length 55, Pred. No. 4.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Behavior; Hydroxylation; Polymorphism; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYDROXYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYDROXYLATION HYDROXYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYDROXYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhodococcus opacus (Nocardia opaca).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1991 (Rel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AE003538; AAF49836.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M21201; AAA28816.1; -. EMBL; X99407; CAA67784.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase; FBgn0003034; Acp70A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X99411; CAA67788.1; -. EMBL; X99413; CAA67790.1; -. EMBL; X99415; CAA67792.1; -. EMBL; X99416; CAA67793.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.8%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6378 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        x99409; CAA67786.1;
x99410; CAA67787.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X99408; CAA67785.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 VAMFLAVAVVLGLATS 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 LALFLVLVCVLGLVQS 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                      (PARAGONIAL GLAND).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X99418; CAA67795.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        255
23
33
33
34
19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A28911; A28911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 AA;
                                                                                                                                                                                                                                                                                                                                                           OVIPOSITION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20
28
33
34
38
38
19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOXU_RHOOP
P22659;
```

S

```
Skovgaard O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RL34_PROMI
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                    NON_TER
DOMAIN
                                                                                                                                                                                                                                                                                                                                 NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proteus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P22836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
RL34_PROMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
      DOR DOR STATE SOLVER SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                       -:- CATALYTIC ACTIVITY: H(2) + NAD(+) = H(+) + NADH.
-:- COFACTOR: BINDS 1 2FE-2S CLUSTER AND 1 4FE-4S CLUSTER (Potential).
-:- SUBUNIT: TETRAMER OF AN ALPHA AND A GAMMA SUBUNITS (FLAVIN-CONTAINING DIMER), AND A DELTA AND A NICKEL-CONTAINING BETA SUBUNITS (HYDROGENASE DIMER).
-:- SUBCELLULAR LOCATION: Cytoplasmic.
-:- SIMILARITY: BELONGS TO THE COMPLEX I 75 KDA SUBUNIT FAMILY.
                                                                                                                                                                                            Zaborosch C., Schneider K., Schlegel H.G., Kratzin H.; "Comparison of the NH2-terminal amino acid sequences of the four non-identical subunits of the NAD-linked hydrogenases from Nocardia opaca ib and Alcaliques eutrobhus H16.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S03945; S03945.
InterPro; IPR000283; Complex1_75K.
PROSITE; PS00641; COMPLEX1_75K_1; PARTIAL.
PROSITE; PS00643; COMPLEX1_75K_2; PARTIAL.
PROSITE; PS00643; COMPLEX1_75K_3; PARTIAL.
Oxidoreductase; Flavoprotein; FMN; Iron-sulfur; 4Fe-4S; NAD; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                        1b and Alcaligenes eutrophus H16.";
Eur. J. Biochem. 181:175-180(1989).
-!- FUNCTION: SUBUNITS ALPHA AND GAMMA OF HOXS CONSTITUTE AN NADH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Francis K.P., Stewart G.S.A.B.;
"Detection and speciation of bacteria through PCR using universal major cold shock protein primer oligomers.";
"Ind. Microbiol. Biotechnol. 19:286-293(1997).
"I. SUBUNIT: HOMODIMER (BY SIMILARITY).
"I. SUBCELLULAR LOCATION: CYCOPIASMIC (By similarity).
"I. INDUCTION: IN RESPONSE TO LOW TEMPERATURE (BY SIMILARITY).
"I. SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
   Actinomyceťales; Corynebacterineae; Nocardiaceae; Rhodococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Photobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB 1; Length 33;
Pred. No. 3.8e+02;
3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 AA; 3492 MW; 62AF6E43F64E719D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Major cold-shock protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-NCIMB 841;
MEDLINE-98101990; PubMed=9439003;
                                                                                                                                                         MEDLINE-89231684; PubMed-2496982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Photobacterium mondopomensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 EGGKATTEEQKLIEDVNA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 44.4v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                  OXIDOREDUCTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                     NCBI_TaxID=37919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=48408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CSPA_PHOMO
Q51929;
                                                                                                                                  STRAIN-1B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
SEQUENCE
                                                                                                   SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CSPA_PHOMO

ID CSPA_PHOMO

OF 15-JUL.

DT 15-JUL.

DT 15-JUL.

DT 15-JUL.

DT 15-JUL.

CSPA.

ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Nucleotide sequence of a Proteus mirabilis DNA fragment homologous to the 60K-rnpA-rpmH-dnaA-dnaN-recF-gyrB region of Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -! - SIMILARITY: BELONGS TO THE L34P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                           Score 37; DB 1; Length 46; Pred. No. 5.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 47;
                                                                                                                                                                                                                                                                                                                                                                                                             6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5494 MW; 6BA887E6E3989394 CRC64;
                                                                                                                                                                                                                                                                                 BD11BC53118B3B5A CRC64
EMBL; U60045; AAC80249.1; -.
HSSP; P32081; ICSP.
HSP: P32081; ICSP.
Fint: PF00113; CSD; 1.
ProDom; P0000621; Cold_shock; 1.
ProDom; P0000621; Cold_shock; 1.
PROATT: R000357; CSP: 1.
Transcription regulation; DNA-binding; Activator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.5%; Score 37; DB 1; I
43.5%; Pred. No. 5.5e+02;
tive 2; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-CCT-1993 (Rel. 27, Last annotation update)
50S ribosomal protein L34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 AA
                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; J00732; J00732.
InterPro; IPR000271; Ribosomal_L34.
Pfam; PF00468; Ribosomal_L34; 1.
PROSITE; PS00784; RIBOSOMAL_L34; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=LM1509;
MEDLINE=91033012; PubMed=2172087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 KATTEEQKLIEDVNASFRAAMAT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KRTFQPSVLKRNRNHGFRARMAT 24
                                                                                                                                                                                                                                                                                                                                                           13.5%;
52.9%;
                                                                                                                                                                                                                                                                                 5021 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M58352; AAA83957.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :|| | || || || 25 SEGFKTLTEGQKVSFDV 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 AEGGKATTEEQKLIEDV 42
                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 43.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                  >46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene 93:27-34(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ribosomal protein.
                                                                                                                                                                                                                                                                              46 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proteus mirabilis
                                                                                                                                                                                                                                    7
                                                                                                                                                                                                                                                         46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=584;
```

```
NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                                            TP0495;
                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
SEQUENCE 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=H37RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y23A MYCTU
P58240;
                                                                        Bacteria;
                                                P0495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y23A_MYCTU
                                                                                                                                                                                                                                                                                                                                                                                              TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                SEQUENCE FROM N.A.

X MEDLINE=92157872; PubMed=1787796;
A Liebetanz R., Hornberger U., Drews G.;
Liebetanz R., Hornberger U., Drews G.;
Liebetanz R., Hornberger U., Drews G.;
T. "Organization of the genes coding for the reaction-centre L and M zerobic photosynthetic bacterium Erythrobacter species OcH114.";
Mol. Microbiol. 5:1459-1468(1991).
-!- FUNCTION: ANTENNA COMPLEXES ARE LIGHT-HARVESTING SYSTEMS, WHICH C.
-!- SUBBUIT: THE EXCITATION ENERGY TO THE REACTION CENTERS.
--- SUBBUIT: THE CORE COMPLEX IS FORMED BY DIFFERENT ALDHA AND BETA CHAINS, BINDING BACTERIOCHLOROPHYLL MOLECULES, AND ARRANGED MOST PROBABLY IN TETRAMERIC STRUCTURES DISPOSED AROUND THE REACTION CENTER. THE NON-PIGMENTED GAMMA CHAINS MAY CONSTITUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PERIPLASMIC (POTENTIAL).
BACTERIOCHLOROPHYLL (POTENTIAL).
MAIAL LIGAND TO THE BACTERIOCHLOROPHYLL
MAGNESIUM (POTENTIAL).
929B906BE4559369 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                          01-MAY-1992 (Rel. 22, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Light-harvesting protein B-870, beta chain (Antenna pigment protein,
                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R PIR; S16309; LBBCB.
R PIR; S16309; LBBCB.
R HSSP, P02951; 1D872
R InterPro; 1PR002362; Antenna_comp_beta.
R InterPro; 1PR002066; LHC.
R Pfan; PF00556; LHC; 1.
R PRIMYS; PR00654; LICHTARNSTB.
R PROSITE; PS00969; ANTENNA_COMP_BETA; 1.
R PROSITE; PS00969; ANTENNA_COMP_BETA; 1.
R Antenna complex; Light.harvesting polypeptide; Transmembrane; Magnesium; Bacteriochlorophyll; Inner membrane.
R PODAMIN 1 CTOPLASMIC (POTENTIAL).
T TRANSMEM 22 44 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                    Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.5%; Score 37; DB 1; Length 49; 69.2%; Pred. No. 5.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 AA.
                      49 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                      Erythrobacter sp. (strain OCh 114)
                                           01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequ
01-FEB-1994 (Rel. 28, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5461 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
44
49
20
38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 MFLAVAVVLGLAT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :| |||||
29 LFAAVAVVAHLAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 AA:
                                                                                                                                                           NCBI_TaxID=2434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1
2
2
3
3
8
                                                                                                beta chain).
                                                                                                                                              Roseobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y495_TREEA
083508;
                     LHB_ERYSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y495_TREPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                         <u>:</u>
                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A D
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-9825597; pubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Edordon S.V., Eiglameier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Woule S., Murphy L., Oliver S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor T., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                         Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artlach P., Bowman C., Cotton M.D., Fujii C., Garland S., Wenter B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 MVAMFLAV----AVVLGLATSPTAEGG-----KATTEEQKLI 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MLLMRLAVPFCRQNAVSSYLALSPLPKGGIFSVALAVSGTAESRCLV 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               al protein; Complete proteome.
49 AA; 5166 MW; 01E3617D5E5DB39C CRC64;
                                                                                                                                                                                                                            Spirochaetales; Spirochaetaceae; Treponema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.5%; Score 37; DB 1; 1 34.0%; Pred. No. 5.7e+02; tive 4; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
10-OCT-2001 (Rel. 40, Last annotation update)
RV0236.1 OR RV0236A OR MT0250.
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein TP0495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98332770; PubMed=9665876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE001226; AAC65490.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spirochete.";
Science 281:375-388(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 16; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                     Treponema pallidum
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1773;
```

^

```
S10315; S10315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Photosystem II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSBI OR SML0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSBI_SYNY3
Q54697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001
                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
PSBI_SYNY3
      PIR;
   DR DR SQ SQ
                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                         SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                          "Whole genome comparison of Mycobacterium tuberculosis clinical and labbratory strains."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
PUTATIVE SECRETED PROTEIN RV0236.1.
006663B2A4756ED9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Photosystem II reaction center I protein (PSII 4.4 kDa protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REACTION CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=9023553; PubMed=2115674;
Chen J.C., Meng B.Y., Fukuta M., Sugiura M.;
"Nucleotide sequence of the psbI gene of the cyanobacterium,
Anacystis nidulans 6301.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 18:4017-4017(1990).
-!- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE REACTION C.
OF PHOTOSYSTEM II, ITS EXACT FUNCTION IS NOT YET KNOWN.
-!- SIMILARITY: BELONGS TO THE PSBI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 AAHKFMVAMFLAVAVVLGLA-----TSPTAEGGKATTEEQKLIEDVNAS 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37; DB 1; Length 57;
Pred. No. 6.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synechococcus sp. (strain PCC 6301) (Anacystis nidulans).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 AAASVVVGLLLGAAAIFGVTLMVQODKKPPLPGGDPSSSVLNRVEYGNRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AL021929; -; NOT_ANNOTATED_CDS. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z92669; -; NOT_ANNOTATED_CDS
EMBL; AE006933; AAK44468.1; ALT_INIT
TIGN MT0250; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.5%;
24.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X52750; CAA36961.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 AA; 5834 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
Nature 393:537-544(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tuberculist; Rv0236A; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
tes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSBI_SYNP6
P17747;
                                                                                                                                                                                                                                                           Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSBI_SYNP6
ID PSBI_SINP6
ID O1-AUG
DT 01-AUG
DT 16-OCT
DE PhotoSI
GN Synech
OC Bacter
OX NCBL_T
RP SEQUEN
RX MEDLIN
RY ANACys
RT ANACys
CC -!- FU
CC -!- SI
CC -!- SI
CC -!- SI
CC -!- SI
CC C -!- SI
CC -!- S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
RREPRESENTATIONS OF THE PROPERTY AND PROPERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-96132547; PubMed-8544827;
IKEUChi M., Shukla V.K., Pakrasi H.B., Inoue Y.;
IKeuchi M., Shukla V.K., Pakrasi H.B., Inoue Y.;
Intercted inactivation of the psbI gene does not affect photosystem
II in the cyanobacterium Synechocystis sp. PCC 6803.";
Mol. Gen. Genet. 249:622-628(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Photosystem II reaction center I protein (PSII 4.4 kDa protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                       5
                                                                                                                                               Length 39;
                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Cyanobacteria; Chrococcales; Synechocystis. NCBL_TaxID=1148;
                                                                                   39 AA; 4392 MW; 17A37C7910211AC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e; Complete proteome.
D1AADF4A59338CD0 CRC64;
                                                                                                                                               Score 36.5; DB 1;
Pred. No. 5.2e+02;
6; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 1; Le
Pred. No. 5.8e+02;
8; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 MVAMFLAVAVVLG------LATSPTAEGGKATTE 34
                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 35, Čreated)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                6 FMVAMFLAVAVVLGLATSPTAEGGKATTEEQKLIED 41
                                                                                                                                                                                                                                                                                                                                                                             38 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Mismatches
                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                             PRT;
InterPro; IPR003686; Psb1.
Pfam; PF02532; Psb1; 1.
Photosystem II: Transmembrane.
TRANSMEM 6 27 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane;
                                                                                                                                               13.3%; 27.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.1%; 26.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U28040; AAC43720.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003686; PsbI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D63999; BAA10085.1;
                                                                                                                                                                  Best Local Similarity 27.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF02532; PsbI; 1
```

Search completed: July 11, 2002, 11:08:23 Job time: 205 sec

Q92sf3 rhizobium m

09ps14 torpedo cal 034026 burkholderi

09x13 Information of the control of

Q91BM0 Q9PSL5 Q9PSL3 Q9UF20 Q9S7U6

Q50345 Q9YYJ5 Q9JHF4

Q9ZIL5 O87300 Q9SAM4

049763 049781 049785

Q9SQE0 Q9SQD3 Q9TX32 Q87306

087405 087411 087414

Q9r554 acinetobact Q87417 chimpanzee Q9ygk6 gadus morhu

```
Diep D.B., Haavarstein S.L., Nissen-Meyer J., Nes I.F.;
"The gene encoding plantaricin A, a bacteriocin from lactobacillus plantarum Cll, is located on the same transcription unit as an agr-like regulatory system."
Appl. Environ. Microbiol. 60:160-166(1994).
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
Lactobacillus.
NCBI_TaxID=1590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96345611; PubMed=8755874;
Diep D.B., Havarstein L.S., Nes I.F.;
Characterization of the locus responsible for the bacteriocin production in Lactobacillus plantarum Cll.";
J. Bacteriol. 178:4472-4483(1996).
EMBL; X94434; CAA64194.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diep D.B., Haavarstein S.L., Nes I.F.;
"A bacteriocin-like peptide induces bacteriocin synthesis in Lactobacillus plantarum Cll.";
Mol. Microbiol. 18:631-639(1995).
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94161498; Pubmed=8117074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C11;
MEDLINE=96414465; PubMed=8817486;
                                                                                                                                                                                                                                                                                                           01-FEB-1997 (TrEMBLrel. 02, 01-FEB-1997 (TrEMBLrel. 02, 01-NOV-1998 (TrEMBLrel. 08,
                                                                                                                                                                                                                                                                                             PRELIMINARY;
Lactobacillus plantarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [3]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
PLNV (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-C11
P71476
P71476;
                                                                                                                                                                                                                                                                                                                                             PLNV
RESULT
P71476
                                                                                                                                                                                                                                                                                                     Q94/2 oryza sativ
Q19186 ovis aries
Q91v94 bos taurus
Q87297 chimpanzee
Q46042 cellulomona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9rs51 deinococcus
Q9zp82 raphanus sa
Q9f5c7 agrobacteri
Q49801 arabidopsis
C17750 caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         045266 bradyrhizob
095826 galaxias sp
0959C8 zea mays (m
098d90 rhizobium 1
                                                     July 11, 2002, 11:04:38; Search time 24.17 Seconds (without alignments) 407.973 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q92q07 rhizobium m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P71476 lactobacill
                                                                                                                                                                                                                                                                                                                                                                                          number of results predicted by chance to have a an or equal to the score of the result being printed, y analysis of the total score distribution.
                                                                                                      57
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                      1 MAAHKFMVAMFLAVAVVLGL.....LIEDVNASFRAAMATTANVP
        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                              562222 segs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                       protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                               P71476
Q45266
Q95826
Q9SQC8
Q98D90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q87297
Q46042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9RS51
Q9ZP82
                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9F5C7
O49801
O17790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9AYH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          092007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         019186
09TV94
                                                                                                                                                                                                                                                                                                                                           sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                            sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                   score greater than or equal to and is derived by analysis of
                                                                                                                                                                                                                                                                                                                                                            sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                   sp_organelle:*
                                                                                      US-09-696-169A-21
275
                                                                                                                                                                                                                                             sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                                                                                        sp_phage: *
sp_plant: *
sp_rodent: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110
110
110
110
110
                                                                                                                                                                                                                                                                                                                                                                           sp_archeap:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
                                                                                                                                                                                                                                                                                                                                    sp_virus:*
                                                                                                                                                                                                                                                                  sp_human:*
                                                                                                                                                                                                                                     SPTREMBL_19:*
                                                                                                                                                                                                                                                              sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                            sb_mhc:*
                                                                                                                                                                              length: 0
length: 57
                                                                                                                                                                                                                                                                                                                                                                                        No. is the name of greater than
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42
42
41.5
41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.5
40
40
40
40
                                                                                                                      Scoring table:
                                                                                                Perfect score:
                                       protein -
                                                                                                                                                                             Minimum DB
Maximum DB
                                                                                                                                                                                                                                     Database :
                                                                                                       Sequence:
                                                                                                                                               Searched:
                                                       Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ٠
9
                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
                                       ĕ
```

Last sequence update)
Last annotation update)

Created)

44 AA.

PRT;

ALIGNMENTS

Q9YGK6

094D47737C3F16B2 CRC64;

```
41 AA; 4516 MW;
                                                                                                                                                                                                                                                                                                                                                                                                   Zea mays (Maize)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
NON_TER
SEQUENCE
    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     098090;
                                                                                                                                                                                                                                                                             09SQC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q98D90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3
                                                                                                                                                                                                                                          4
                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              060860
                                                                                                                                                                                                                                                           09SQC8
                                                                                                                                                                                                                                                                                                   S
                                                                                                                                          õ
                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                      ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-POOLBURN TRIBUTARY, CLUTHA SYSTEM;
MEDLINE-2123812: PubMed-11327165;
Waters J.M., Wallis G.P.;
"Cladogenesis and loss of the marine life-history phase in freshwater galaxiid fishes (Osmeriformes: Galaxiidae).";
EVOLUTION 55:587-597(2001).
EMBL; AF267389; AAK53197.1; -.
MILCOCHONDION.

NON_TER

41 41
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-93043496; PubMed-1421512;
Goettfert M., Holzhaeuser D., Baeni D., Hennecke H.;
"Structural and functional analysis of two different nodD genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Osmeriformes; Galaxiidae; Galaxias.
NCBI_TaxID=126351;
                                                                                                                                                                                                                                                                                                                                                                                                                                Bradyrhizobium japonicum.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bradyrhizobium group; Bradyrhizobium.
                                                                                                                      3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                               Length 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.0%; Score 44; DB 2; Length 44; 38.1%; Pred. No. 3.2e+02;
                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Indels
                    BF82B6E1AE9CB70E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 44 AA; 4767 MW; 2CCDC0F48A0A4422 CRC64;
                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NODULATION PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             095826;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NADH DEHYDROGENASE SUBUNIT 6 (FRAGMENT).
                                                                           Score 44.5; DB 2;
Pred. No. 2.8e+02;
6; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bradyrhizobium japonicum.";
Mol. Plant Microbe Interact. 5:257-265(1992).
Mol.TER 44 44 44
                                                                                                                                                                                                                                                                                                   44 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                               5 KFMVAMFLA---VAVVLGLATSP 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34
  44
4853 MW;
                                                                           Query Match 16.2%;
Best Local Similarity 43.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : : : | |||||| : |
14 LAMNIAVSPTAEGSSGRAQVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 VVLGLATSPTAEGGKATTEEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 38.1.
** A Conservative # Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'poolburn'.
                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
44
44 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Galaxias sp.
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                  045266;
                                                                                                                                                                                                                                                                                             045266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        928260
                                                                                                                                                                                                                                                        N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
095826
                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                           045266
FT
                                                                                                                                                             δ
                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

```
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE FROM N.A.
STRAIN=CV. INBRED B73;
MEDLINE=99403018; PubMed=10471724;
Rabinowicz P.D., Braun E.L., Wolfe A.D., Bowen B., Grotewold E.;
"Maize R2R3 Myb genes. Sequence analysis reveals amplification in the higher plants.";
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
NCBL_TaxID=381;
                                                     ..
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
     Length 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 43;
                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 AA; 4979 MW; D3C22C98D96CC597 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0cT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
MSR4809 PROTEIN.
MSR4809.
                                                                                                                                                                                                                                                                                           0950C8;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
R2R3MYB-DOMAIN PROTEIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42; DB 10; L
Pred. No. 5.5e+02;
4; Mismatches 8;
Score 42.5; DB 8;
Pred. No. 4.5e+02;
7; Mismatches 17;
                                                                                                  6 FMVAMFLAVAVVLGLATSPTAEGGKATTEEQKLIEDVNAS 45
                                                                                                                              43 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-MAFF303099;
MEDLINE-21082930; PubMed-11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro IPR001005; Myb_DNA_bind.
Pfan; PF000249; Myb_DNA_binding; 1.
SMART; SM00395; SANT; 1.
PROSITE; PS50090; MYB_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               higher plants.";
Genetics 153:427 444(1999).
EMBL; AF099391; AAF04666.1; -.
HSSP; Q03237; 1ASJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | | |: | ||:||| ::|
6 PDIRRGRFTAEEEKLIISLHA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.3%;
     Query Match 15.5%;
Best Local Similarity 32.5%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 PTAEGGKATTEEQKLIEDVNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Conservative
                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 9; Conservat
```

 $\sim$ 

ö

```
Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ovis aries (Sheep).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=DORSET DOWN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                              NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998
01-JAN-1998
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   019186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            019186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QQ
                                                                                                                                                                                                                                                                                                                     ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Galibert F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F., Barloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G., Barloy-Hubler F., Buhrmester J., Cadieu E., Capela D., Chain P., Cowle A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F., Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M., Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D., Kahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V., Masuy D., Palm C., Peck M.C., Pohl T.M., Portetelle D., Purnelle B., Vorhoelter F.J., Weidner S., Wells D.H., Wisk K., Yeh K.-C., Batut J.; Science 29::668-672(2001).

EMBL: AL591787; CAC46132.1; -
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ů,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41.5; DB 16; Length 52; Pred. No. 7.8e+02;
                                                                                                                                                                                                                                                                           44;
                                                                                                                                                                                                                                                                                                                     11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; Complete proteome.
SEQUENCE 52 AA; 5348 MW; 23817E5136689924 CRC64;
                                                                                                                                                                                                      44 AA; 5123 MW; 4BE68A9AEBE1107B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) HYPOTHETICAL TRANSMEMBRANE PROTEIN SMC01239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 4.0 KDA PROTEIN.
OSJNBA0087H07.12.
                                                                                                                                                                                                                                                                    Ouery Match , 15.3%; Score 42; DB 16; Best Local Similarity 43.5%; Pred. No. 5.6e+02; Matches 10; Conservative 2; Mismatches 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KFMVAMFLAVAVVLGLATSPTAEGGKATTEEQ 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mesorhizobium loti.";
DNA Res. 7:31-338(2000).
EMBL, AP003005; BAB51381.1; -
InterPro; IPR000271; Ribosomal_L34.
Pfam; PF00466; Ribosomal_L34; 1.
Complete proteome.
SEQUENCE 44 AA, 5123 MW; 4BE68A9A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q92Q07;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=1021;
MEDLINE=21368234; PubMed=11474104;
                                                                                                                                                                                                                                                                                                                                                            30 KATTEEQKLIEDVNASFRAAMAT 52
                                                                                                                                                                                                                                                                                                                                                                                                        2 KRTYQPSKLVRKRRHGFRARMAT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.1%;
40.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 13; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9AYH2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9AYH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    092007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESCULT
1092007
1092007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
100307
1003007
1003007
1003007
1003007
1003007
1003007
1003007
1003007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   099XYZ
ID 099
AC 099
DT 011
DT 011
DE HX
GN OS
    RA
RT
RT
DR
DR
SQ
SQ
                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Eukaryota; Viridipiantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazóa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-DORSET DOWN;
Palmer B.R., Roberts N., Kent M.P., Ilian M.A., Le Couteur C.E.,
Morton J.D., Hickford J.G.H., Bickerstaffe R.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5;
                                                                                             Ж.,
                                                                                                                                                                                                                                                                                              Length 39;
                                                                                                                                                                                                                                                                                                                                  10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [3]
SEQUENCE FROM N.A.
SEQUENCE TOWN;
Palma-DORSET DOWN;
Palma B.R., Roberts N., Hickford J.G.H., Bickerstaffe R.
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF016008; AAD04196.1;
EMBL; AF016006; AAB88415.1;
EMBL; AF016007; AAB88416.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 AA; 4954 NW; A5AF7FDAD7CCCDAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96314779; PubMed=8759125;
Roberts N., Palmer B., Hickford J.G., Bickerstaffe
"PCR-SSCP in the ovine calpastatin gene.";
Anim. Genet. 27:211-211(1996).
                                                                                                                                                                                                                                                                                          Score 41; DB 10;
Pred. No. 6.5e+02;
6; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB 6;
Pred. No. 7.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 TSPTAEGGKATTEEQKLIEDVNASFRAAMATTANVP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                              9 VOLLLVLFVLLAFASGILAQGGPST 33
                                                                                                                                                                                                                                                                                                                                                                        8 VAMFLAVAVVLGLATSPTAEGGKAT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 05, C
(TrEMBLrel. 05, I
(TrEMBLrel. 08, I
                                                                                                                                                                                                                                                                                            14.9%;
36.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.9%;
ilarity 33.3%;
Conservative
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 36.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CALPASTATIN (FRAGMENT).
```

ï

```
55 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                        Cellulomonas fimi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                34
55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                            Signal.
SIGNAL
                                      Q46042
Q46042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09RS51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9RS51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
RESULT 11
                    046042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9RS51
                                                            ACCOOR BELL REPORTED BY THE REPORT OF THE RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Palmer B.R., Su H.-Y., Roberts N., Hickford J.G.H., Bickerstaffe R.; "Single Nucleotide Polymorphisms in an Intron of the Ovine Calpastatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                          Bos taurus (Bovine).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-ANE;
MEDLINE-94246762; PubMed-8189548;
Chackerian B., Morton W.R., Overbaugh J.;
"Persistence of simian immunodeficiency virus Mne variants upon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.9%; Score 41; DB 15; Length 53; larity 40.7%; Pred. No. 9.1e+02; Conservative 3; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 49;
                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF117813; AAD21054.1; -.
NON_TER 1 1 1
NON_TER 49 49
SEQUENCE 49 AA: 4992 MW; 54941AC8BFA32362 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 AA; 5587 MW; 003E55865FDEFF27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ENVELOPE GLYCOPROTEIN (FRAGMENT).
                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimpanzee immunodefictency virus (SIV(cpz)) (CIV).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB 6; Pred. No. 8.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.9%; Sco. 33.3%; Pred. No. 6...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 TSPTAEGGKATTEEQKLIEDVNASFRAAMATTANVP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 GLATSPTAEGGKATTEEQKLIEDVNAS 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transmission.";
J. Virol. 68:4080-4085(1994).
EMBL; UG6278, AAA20249.1; -.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
                                                                    01-MAY-2000 (TrEMBLrel. 13, 0
01-MAY-2000 (TrEMBLrel. 13, 1
01-MAY-2000 (TrEMBLrel. 13, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 33.3
nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                      PRELIMINARY;
                                                                                                                                  CALPASTATIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=11723;
                                                                                                                                                                                                                                                    NCBI_TaxID-9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     087297
087297;
                                                    Q9TV94;
                                  Q9TV94
σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
Q87297
RESULT
                    09TV94
                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

```
ö
                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
Owolabi J.B., Beguin P., Kilburn D.G., Miller R.C. Jr., Warren R.A.J.;
Owolabi J.B., Beguin P., Kilburn D.G., Miller R.C. Jr., Warren R.A.J.;
Expression in Escherichia coli of the Cellulomonas fimi structural
gene for endoglucanase B.";
Appl. Environ. Microbiol. 54:518-523(1988).
EMBL: M33025, AAA23085.1; -.
HSSP; P26221; ITF4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=RI;
MEDLINE-20036896; PubMed-10567266;
White O. Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Richardson D.L.,
Dodson R.J., Haft D.H., Guinn M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterboack T., Zalewski C.,
Wakarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                               Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Micrococcineae; Cellulomonadaceae; Cellulomonas. NCBI_TaxID=1708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deinococcus radiodurans.
Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
NCBL_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.9%; Score 41; DB 2; Length 55; 40.0%; Pred. No. 9.5e+02; Live 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR; DR2276; -.
Hypothetical protein; Complete proteome.
SEQUENCE 49 AA; 5071 MW; 83A28B018D2EB501 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37B3CCD04A72393D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 5.1 KDA PROTEIN.
                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40.5; DB 16;
Pred. No. 9.6e+02;
                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence upc
01-DEC-2001 (TrEMBLrel. 19, Last annotation upc
enpogluCANASE B (CENB) PRECURSOR (FRAGMENT).
      ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001701; Glyco_hydro_9.
Pfam; PF00759; Glyco_hydro_9; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 MVAMFLAVAVVLGLATSPTAEGGKA 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55
5608 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                radiodurans R1.";
Science 286:1571-1577(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.7%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE002060; AAF11832.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 40.0%
Matches 10; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33
>55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
```

```
Yoshida K.;
                                                                                                                                                                                                                                           rhizogenes.
                                                                                                                                                                                                                                                                                                       Plasmid.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        049801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATMYB79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                049801
                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
049801
    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                        Raphanus sativus (Radish).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Erassicales; Brassicaceae; Raphanus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moriguchi K., Maeda Y., Satou M., Kataoka M., Tanaka N., Yoshida K.; "Analysis of unique variable region of a plant root inducing plasmid, PR11724, by the construction of its physical map and library."; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-MAFF03-01724;
Moriguchl K., Maeda Y., Satou M., Satuti N., Kataoka M., Tanaka N.
Yoshida K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete nucleotide sequence of a Ri (root inducing) plasmid indicates its chimerical structure between Ti and Sym plasmids."; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Rhizobium.
    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=MAFF03-01724;
Moriguchi K., Nishida T., Maeda Y., Tanaka N., Yoshida K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 37;
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Baymiev A.K., Gimalov F.R., Vakhitov V.A.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ132903; CAB39172.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D7A14C4606C28311 CRC64;
                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
    3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40; DB 10;
Pred. No. 8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ¥
                                                                                                                                                                                             ¥
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                             37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 TAEGGKATTEEQKLIEDVNASFRAAMATT 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 TAAGASAQTAGQKISESAEAAVNVVKEKT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
    .,
                                                                                                                                                                                                                                                                                                COLD SHOCK PROTEIN (FRAGMENT) CSP5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.5%;
34.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 37
37 AA; 3575 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16,
                                         10 MFLAVAVVLGLATSPTA 26
                                                                    :|| ||:| ||:|
16 IFLVVALVWGM-TGPTA 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 14.5
Best Local Similarity 34.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agrobacterium rhizogenes.
10; Conservative
                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=MAFF03-01724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIORF125 PROTEIN RIORF125.
                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid pRi1724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
                                                                                                                                                                                                                 Q9ZP82;
                                                                                                                                                                                           092P82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9F5C7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
09F5C7
AC 09F5C7
AC 09F5C7
DT 01-MAR
OC Bacter
CO Bacter
                                                                                                                                                   13
  Matches
                                                                                                                                          RESULT
092283
092842
0092782
0092782
0092782
0092782
0092782
0092782
0092782
0092782
0092782
0092782
0092782
0092782
0092782
0092782
0092782
0092782
0092782
0092782
0092782
0092782
0092782
0092782
0092782
0092782
0092782
                                         õ
                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Romero I., Fuertes A., Benito M.J., Malpica J., Leyva A., Paz-Ares J.;
"One hundred R2R3-MYB genes in the genome of Arabidopsis thaliana.";
submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, 295802; CAB09234.1; -.
HSSP; Q03237; 1A5J.
                                                                                                                                                                                                               plasmid (1): Sequencing analysis of T-DNA and pRi1724 in Japanese Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
"Genome structure of Ri plasmid (1):Construction of linking library and physical map of pRi1724 in Japanese Agrobacterium."; Nucleic Acids Symp. Ser. 39:189-190(1998).
                                                                                                                                                                   Maeda Y., Moriguchi K., Kataoka M., Satou M., Satuti N., Tanaka N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.5%; Score 40; DB 10; Length 45; 29.0%; Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Indels
                                                                                                                                                                                                                                                                                                                                                            E9B74EBFB795D0A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C4F16570A5772049 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                 14.5%; Score 40; DB 2; 39.4%; Pred. No. 8.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1998 (TrEMBLrel. 06, Last sequence 01-DEC-2001 (TrEMBLrel. 19, Last annotation RAR3-MYB TRANSCRIPTION FACTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45
                                                                                                                                                                                                                                                                                      Nucleic Acids Symp. Ser. 42:67-68(1999).
EMBL; AP002086; BAB16244.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 PTAEGGKATTEEQKLIEDVNASFRAAMATTA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 MVAMFLAVAVVLGLAT --- SPTAEGGK - ATTEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          completed: July 11, 2002, 11:08:07 ne: 209 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                               SEQUENCE FROM N.A.
STRAIN-MAFF03-01724;
MEDLINE-20241294; PubMed-10780382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001005; Myb_DNA_bind.
Pfam; PF00249; myb_DNA-binding; 1.
PROSITE; PS50090; MYB_3; 1.
                                                                                                                                                                                                                                                                                                                                                          38 AA; 3711 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1998 (TrEMBLrel. 06,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5351 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                               "Genome structure of Ri
its flanking regions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
es 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45
```

Human 5' EST secre Human secreted pro Human cytomegalovi Peptide #5051 enco Peptide #5114 enco Recombinant-derive

Sequence encoded b

C-terminus of myc-

Graminae pollen al

```
Lolium perenne Lol pV and Dactylis glomerata Dac gV epitope(s) and DNA - for treating sensitivity to rye-grass pollen allergen or an immunologically cross-reactive allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lolium perenne; Lol pV; Dactylis glomerata; Dac gV; epitope; sensitivity; ryegrass pollen allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPIX-3, peptide fragment of Lol pV protein allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                               AAW07320
AAY12699
                                                                                               AAY86235
AAB86663
                                                                                                                                                          AAR07270
AAB38350
AAW19369
                                                                                                                                                                                                                          AAU16602
AAW76458
AAG77424
AAR82536
                                                                                                                                                                                                                                                                                          AAG47131
AAR89396
AAP70040
                                                                                                                                                                                                                                                                                                                                         AAU67017
AAU54696
                                                                                                                                                                                                                                                                                                                                                                                                       ABB20298
AAM55691
AAM15893
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM28401
AAM03628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR82539
ABG19054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG22556
AAY91545
                                                                                                                                                                                                                                                                                                                                                                           ABB29709
                                                                                                                               AAM18617
                                                                                                                                              AAM31077
                                                                                                                                                                                                                                                                                                                                                                                        ABB34881
                                                                              AAP40042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR71510 standard; Protein; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kuo M, Luqman M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 2; 110pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IMMU-) IMMULOGIC PHARM CORP
 94WO-US09024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93US-0106016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-NOV-1995 (first entry)
 WPI; 1995-115444/15.
Lolium perenne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Griffith IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9506728-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-MAR-1995
                                                                                                                                                                                                                                                                                                         0.044
0.004
0.004
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.000
0.
 AAR71510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR71510
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPIX-3, peptide fr
LPIX-4, peptide fr
Kentucky Blue Gras
Graminae pollen al
Graminae pollen al
Kentucky Blue Gras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A_Geneseq_032802:*

| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
| SIDS1/gcgdata/hold-geneseqy-embl/AA1991.DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*
| SIDS1/gcgdata/hold-geneseqy-embl/AA1995.DAT:*
| SIDS1/gcgdata/hold-geneseqy-embl/AA1995.DAT:*
| SIDS1/gcgdata/hold-geneseqy-embl/AA1995.DAT:*
| SIDS1/gcgdata/hold-geneseqy-embl/AA1995.DAT:*
| SIDS1/gcgdata/hold-geneseqy-embl/AA1995.DAT:*
| SIDS1/gcgdata/hold-geneseqy-embl/AA1995.DAT:*
                                                                                                                          (without alignments)
213.603 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPIX-2.1, peptide
Rice beta-glucanas
Eucalyptus grandis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCR alpha chain pe
Graminae pollen al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:*/SIDS1/gcgdata/hold-geneseqy/geneseqp-emb1,AA1999.DAT:*/SIDS1/gcgdata/hold-geneseqy/geneseqp-emb1,AA2000.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                        US-09-696-169A-21
275
1 MAAHKFWVAMFLAVAVVLGL......LIEDVNASFRAAMATTANVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                           July 11, 2002, 11:01:03; Search time 29.64 Seconds
                                                                                                                                                                                                                                                                                                                        375566
               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                        747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                           protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR71510
AAR89385
AAW76455
AAW76456
AAR89386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR71509
AAY09286
AAB33392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR62917
AAW76454
                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16
117
117
119
119
220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length: 0
length: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229.8
223.6
223.6
223.6
223.6
119.3
119.3
117.8
117.5
```

82 71 71 53 53 53 48 48

Score

Result . 9

Secretory signal s Propionibacterium Propionibacterium Peptide #2360 enco Peptide #2387 enco

sed

8 0 0 0

Minimum I Maximum I

Database

Title: Perfect score:

Sequence:

ı

protein

ŏ

Run on:

Scoring table:

Searched:

Kentucky Blue Gras Secretory signal s

Human brain expres Peptide #2327 enco Peptide #2438 enco Peptide #2310 enco

IA beta chain frag Novel human diagno Zea mays protein f Human secreted pro

Protein #2297 enco

Human novel secret Graminae pollen al Human colon cancer IA beta chain frag Arabidopsis thalla

Human secreted pro Beta 7 integrin Rl Beta 7 integrin su

\*88888888888

```
Peptide including at least 1 human antigenic determinant of Kentucky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present peptide is a human antigenic determinant contg. peptide, comprising residues 29-48 of the recombinant Kentucky Blue Grass pollen allergen rKBG60, which is from the Poa p IX gp. of grass pollen allergens. A compsn. comprising the peptide and a carrier can be used to desensitise allergic individuals, and prevent allergic individuals from developing an allergic reaction to grass pollen. The compsn. may also be used to deplete allergen specific antibody producing cells. The peptide can be used to diagnose grass pollen allergy, and has the following human immunological response profile, B-cell (HIGG (+)/HIGE (-)), T-cell (+).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blue Grass allergen - from Poa p IX 9p. of grass pollen allergens, used to desensitise allergic individuals, prevent grass pollen allergy and deplete allergen-specific antibodies
                                                                                                                                                                                                                                                           Antigenic determinant; recombinant; Kentucky'Blue Grass; pollen;
                                                                                                                                                                                                                                                                             allergen; antigenic; rKBG60; Poa p IX group; desensitisation; allergic; allergy; prevention; development; reaction; grass; antibody; anergise; producing cell; diagnosis; human; clone 60; immunological response; B-cell; higG; higE; T-cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 17; Length 20;
                                                                                                                                                                                                                      Kentucky Blue Grass pollen allergen rKBG60 resides 29-48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 65; DB 17
Pred. No. 0.039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 AA.
                                                                                                  Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Page 29; 59pp; English.
                                                                                                20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.6%;
66.7%;
20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95WO-CA00439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94US-0280455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide;
                                                                                              AAR89385 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||||:||||||| :| |:
3 kattdeqkliekinvgfk 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 KATTEEQKLIEDVNASFR 47
egklledvnagfkaavaaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 23.6
Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYMA-) UNIV MANITOBA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-116753/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW76455 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 AA;
                                                                                                                                                                                                                                                                                                                                                                                  Poa pratensis
                                                                                                                                                                                                                                                                                                                                                                                                                       WO9603106-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUL-1994;
                                                                                                                                                                              17-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mohapatra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW76455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                       AAR89385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW76455
                                                                          AAR89385
                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                     à
                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
            Lol pV, is a major allergen of ryegrass pollen, and is encoded by the cDNA sequence of clone 12R (AAQ85932), a full-length clone derived from a lambda gtll library. Peptides (AAR71508-61) comprising at least one T cell epitope derived from the Lol pV protein are claimed, and can be used to treat or diagnose sensitivity to ryegrass pollen in an individual or to pollen proteins that are immunologically related to Lol pV, such as Dac gV (see AAR71507).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lol pV, is a major allergen of ryegrass pollen, and is encoded by the colons sequence of clone 12R (AAQ8592), a full-inorth clone derived from a lambda gill library. Peptides (AAR71508-61) comprising at least one T cell epitope derived from the Lol pV protein are claimed, and can be used to treat or diagnose sensitivity to ryegrass pollen in an individual or to pollen proteins that are immunologically related to Lol pV, such as Dac gV (see AAR71507).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lolium perenne Lol pV and Dactylis glomerata Dac gV epitope(s) and DNA - for treating sensitivity to rye-grass pollen allergen or an immunologically cross-reactive allergen.
                                                                                                                                                                                                                                                                                 ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lolium perenne; Lol pV; Dactylis glomerata; Dac gV; epitope; sensitivity; ryegrass pollen allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 71; DB 16; Length 20;
Pred. No. 0.0058;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                      DB 16; Length 20; 0.00017; ches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPIX-4, peptide fragment of Lol pV protein allergen.
                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                        Score 82;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 2; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
m
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR71511 standard; Protein; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Luqman M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.8%;
70.0%;
                                                                                                                                                                                                                                      29.8%;
84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IMMU-) IMMULOGIC PHARM CORP.
                                                                                                                                                                                                                                                                                                                                         94WO-US09024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93US-0106016
                                                                                                                                                                                                                                                                                                                    26 AEGGKATTEEQKLIEDVNA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kuo M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-115444/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 AA;
                                                                                                                                                                            20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lolium perenne.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Griffith IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9506728-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR71511;
                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
```

~

ò g

**AAR71511** RESULT

ö

Gaps

ö

11-DEC-1998 (first entry)

EQKLIEDVNASFRAAMATTA

35

ò

45.0%; Pred. No. 3.4;

```
Best Local Similarity
Matches 9; Conserv
                                                                                                8
                                                                                                  RESULT
AAW76454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR71509
                                                                                                                                                   U.
                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                      ò
                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                              Gaps
      comprising residues 39-58 of the recombinant Kentucky Blue Grass pollen allergen rKBG60, which is from the Poa p IX gp. of grass pollen allergen rKBG60, which is from the Poa p IX gp. of grass pollen allergens. A compan. comprising the peptide and a carrier can be used to desensitise allergic individuals, and prevent allergic individuals from developing an allergic reaction to grass pollen. The compan. may also be used to deplete allergen specific antibodis from an individual, and anergise allergen specific antibody producing cells. The peptide can be used to diagnose grass pollen allergy, and has the following human immunological response profile, B-cell (higG (-)/higE (-)), T-cell (-).
present peptide is a human antigenic determinant contg. peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibody production against allergenic antigen (Ag) is specifically suppressed by treatment with the junctional segment of the alpha and/or beta chain of the Ag receptor of suppressor T (Ts) cells (TCR) induced by tolerogenic Ag-PEG conjugates. Induction of antigen-specific suppression by treatment of mice with TCR alpha-chain peptides was demonstrated using the peptides given in AAR62912-17. The peptide of AAR62917 was used as a control.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     effecting immuno:therapy - have an amino a portion of the CDR3 region of a T-cell
                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                                                                                                                                     complementarity determining region; immunosuppressive; antibody engineering; suppressor T-lymphocyte; Ts; ovalbumin;
                                                                                                                                                                                    Score 53; DB 17; Length 20; Pred. No. 1.8;
                                                                                                                                                                                                             7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Allergen; immunotherapy; T-cell receptor; TCR; CDR;
                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 44; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             monoclonal antibody; myeloma; IgG.
                                                                                                                                                                                                                                                                                                                         AAR62917 standard; Protein; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                 TCR alpha chain peptide control.
                                                                                                                                                                                    19.3%;
50.0%;
                                                                                                                                                                                                                                                   ||| :| |:||:| ||
| liekinvgfkaavaaaggvp 20
                                                                                                                                                                                                                                      57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93GB-0008581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94WO-CA00228
                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                     38 LIEDVNASFRAAMATTANVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for
                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acid sequence comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYMA-) UNIV MANITOBA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic peptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1994-358193/44.
                                                                                                                                                                              Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mohapatra SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                         12-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9425489-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                  AAR62917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor
 The
                                                                                                                                                                                                                                                                                                             AAR62917
                                                                                                                                                                                                                                                                                                 RESULT
8888888888888
                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                           Dp
```

DB 15; Length 20;

Score 51;

18.5%;

Query Match

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW76449-W76534 are peptide fragments of a natural pollen allergen, Phl p 5b, isolated from Graminae species. This allergen can be modified and the reactivity of the modified allergens with IgE antibodies to grass pollen allergens is reduced or eliminated while their reactivity with T cells is retained. The genes for the allergens are modified so that the encoded polypeptides have one or more amino acid substitutions, deletions and/or additions. The dominant T-cell epitopes of the allergens are not genetically altered. Such allergens have applications in the immunotherapy of allergies e.g. hyposensitisation.
                                                                                                                                                                                                                                                                                                                                                                                                       Pollen; allergen; Phl p 5b; IgE; antibody; grass; reactivity; T cell; epitope; immunotherapy; allergy; hyposensitisation.
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified recombinant allergens - useful for immuno-therapy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.8%; Score 49; DB 19; Length 12; 100.0%; Pred. No. 3.3; tive 0; Mismatches 0; Indels
  Indels
                                                                                                                                                                                                                                                                                                                                                        Graminae pollen allergen Phl p 5b peptide fragment #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jaeger L;
7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fiebig H,
Stuewe F
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR71509 standard; Protein; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Becker W, Bufe A, Cromwell O, F
Kahlert H, Mueller W, Schramm G,
                                                                                                                                                                                                              AAW76454 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 12; 31pp; German.
                                              57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97DE-1013001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97DE-1013001.
                                                                       :|| :| |:||:|
| miekinvgfkaavaaaggvp
                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-NOV-1995 (first entry)
                                              38 LIEDVNASFRAAMATTANVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 100.
Matches 10; Conservative
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-522170/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 GKATTEEOKL 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DE19713001-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-MAR-1997;
                                                                                                                                                                                                                                                                                                         11-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           allergies
                                                                                                                                                                                                                                                             AAW76454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Graminae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR71509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            XIXX
```

m

us-09-696-169a-21.closed.rag

```
(MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Poa pratensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9603106-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mohapatra SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-FEB-1996.
                   Becker W,
Kahlert H,
                                                                              allergies
                                                                                                                                                                                                                                                                                                                                                                       AAR89386;
                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                           AAR89386
                                                                                                                                                                                                                                                                                                                                                               Q
                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                    AAW76449-W76534 are peptide fragments of a natural pollen allergen, phl p 5b, isolated from Graminae species. This allergen can be modified and the reactivity of the modified allergens with Tge antibodies to grass pollen allergens is reduced or eliminated while their reactivity with T cells is retained. The genes for the allergens are modified so that the encoded polypeptides have one or more amino acid substitutions, that the encoded polypeptides have one or more amino acid substitutions, deletions and/or additions. The dominant T-cell epitopes of the allergens are not genetically altered. Such allergens have applications in the immunotherapy of allergies e.g. hyposensitisation.
                            Pollen; allergen; Phl p 5b; 1gE; antibody; grass; reactivity; T cell; epitope; immunotherapy; allergy; hyposensitisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pollen; allergen; Phl p 5b; 1gE; antibody; grass; reactivity; T cell; epitope; immunotherapy; allergy; hyposensitisation.
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                       Modified recombinant allergens - useful for immuno-therapy of
                                                                                                                                                                                                                                                                                                                                                                                                 21.1%; Score 58; DB 19; Length 12; 100.0%; Pred. No. 0.19; ive 0; Mismatches 0; Indels
        Graminae pollen allergen Phl p 5b peptide fragment #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Graminae pollen allergen Phl p 5b peptide fragment #8.
                                                                                                                                                                          Jaeger L;
                                                                                                                                                                         Fiebig H, Stuewe H;
                                                                                                                                                                         Bufe A, Cromwell O, F
Mueller W, Schramm G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW76456 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                     Example 1; Page 12; 31pp; German.
                                                                                                                 97DE-1013001.
                                                                                                                                   97DE-1013001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97DE-1013001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97DE-1013001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                     (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                    12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 KATTEEQKLIED 41
                                                                                                                                                                                                    WPI; 1998-522170/45.
                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                           allergen;
                                                                                                                                                                                                                                                                                                                                                                       12 AA;
                                                                          DE19713001-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DE19713001-A1
                                                                                                                27-MAR-1997;
                                                                                                                                   27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-DEC-1998
                                                                                             01-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1998
                                                                                                                                                                                   Kahlert H,
                                                                                                                                                                         Becker W,
                                                                                                                                                                                                                                  allergies
                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW76456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Graminae
                                                         Graminae
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
AAW76456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

```
Philosophy isolated from Graminas meets. This allefon can be modified and the reactivity of the modified allergens with IgE antibodies to grass pollen allergens is reduced or eliminated while their reactivity with T cells is retained. The genes for the allergens are modified so that the encoded polypeptides have one or more amino acid substitutions, deletions and/or additions. The dominant T-cell epitopes of the allergens are not genetically altered. Such allergens have applications in the immunotherapy of allergies e.g. hyposensitisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide including at least 1 human antigenic determinant of Kentucky Blue Grass allergen - from Poa p IX gp. of grass pollen allergens, used to desensitise allergic individuals, prevent grass pollen allergy and deptete allergen-specific antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                      AAW76449-W76534 are peptide fragments of a natural pollen allergen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antigenic determinant; recombinant; Kentucky Blue Grass; pollen, allergen; antigenic; rKBG60; Poa p IX group; desensitisation; allergic; allergy; prevention; development; reaction; grass; antibody; anergise; producting cell; diagnosis; human; clone 60; immunological response; B-cell; hIgG; hIgE; T-cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                             Modified recombinant allergens - useful for immuno-therapy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kentucky Blue Grass pollen allergen rKBG60 resides 39-58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
   ï
   Jaeger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 53; DB 19;
Pred. No. 0.91;
1; Mismatches 0;
Fiebig H,
Stuewe H;
Bufe A, Cromwell O, Fi
Mueller W, Schramm G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR89386 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 5; Page 29; 59pp; English
                                                                                                                                                                                                                                                     Example 1; Page 12; 31pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.3%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95WO-CA00439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94US-0280455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-SEP-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 90.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYMA-) UNIV MANITOBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-116753/12.
                                                                                              WPI; 1998-522170/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 TEEQKLIEDVN 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 AA;
```

ö

S

```
beta guedanes gene. Also described are: (A) a connective cut beta guedanes gene. Also described are: (A) a connective described are transgenic monocot plant, comprising: (i) a transcriptional regulatory region which hybridises under high stringency with a rice beta cylucanase promoter; and (ii) a DNA sequence heterologous to the cregulatory region, and encoding a protein to be produced by the plant; and (iii) a second DNA sequence encoding a signal polypeptide operatively confliked 5' to 3', so that the signal polypeptide is in translation frame with the protein, and is effective to facilitate secretion of the protein caross aleurone or soutellar epithelium layers into the endosperm of seeds obtained from the plant; (B) a menocot plant stably transformed with CG1: (C) seeds from the above plant; (D) a method of enhancing the resistance of a monocot plant to fungal infection by stably transforming catably transforming a plant with CG1: Obtaining seeds from the transforming a plant with CG1. Obtaining the protein from the seed endosperm; (F) an isolated protein having the characteristics of a rice beta-glucanase enzyme, corresponding to beta-glucanase enzyme, corresponding to beta-glucanase enzyme, corresponding to beta-glucanase enzyme, corresponding to beta-glucanases enzyme, corresponding to pera-glucanases and plants. The polynucleotides of the invention are useful to transform corporate increased resistance to fungal infection, improved growth corporate increase obtained from the plant.
                                                                                                                                                                                                                             polynucleotides (PN) comprising
                                                                                                                                                                                                                                             a sequence which hybridises under high stringency with a rice
beta-glucanase gene. Also described are: (A) a chimeric gene (CG1) used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant; transcription factor; gene expression; eucalyptus; pine; acacia; poplar; sweetgum; teak; mahogany; bZIP; G-box bliding factor; basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS; homeodomain; zipper; LIM domain; AP2; EREBS; zinc finger domain;
                                                                                      New polynucleotides which hybridise with rice beta-glucanase genes useful for transforming monocot plants for various characteristics including increased resistance to fungal infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eucalyptus grandis transcription factor protein sequence #458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 48; DB 20; Length 27;
Pred. No. 13;
3; Mismatches 7; Indels
                                                                                                                                                                                                                        present invention describes isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    type 2 Cys2His2; CCAAT box element; MYB.
                                                                                                                                                                           Disclosure; Page 39; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB33392 standard; Protein; 56 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAAHKFMVAMFLAVAVVLGLATSPT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.5%;
52.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-MAR-2000; 2000WO-US061.12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0266513.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 52.0
Matches 13; Conservative
                           WPI; 1999-105620/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eucalyptus grandis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 AA;
                                               N-PSDB; AAX33549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200053724-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-MAR-1999;
18-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB33392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB33392
      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lol pV, is a major allergen of ryegrass pollen, and is encoded by the colon Sequence of clone 12R (AAQ8532), a full-length clone derived from a lambda gtll library. Peptides (AAR71508-61) comprising at least one T cell epitope derived from the Lol pV protein are claimed, and can be used to treat or diagnose sensitivity to ryegrass pollen in an individual or to pollen proteins; that are immunologically related to Lol PV, such as Dac gV (see AAR71507).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rice; beta-glucanase; Gns; promoter; plant resistance; expression; fungal infection; transgenic monocotyledon; growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lolium perenne Lol pV and Dactylis glomerata Dac gV epitope(s) and DNA - for treating sensitivity to rye-grass pollen allergen or an immunologically cross-reactive allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                    Lolium perenne; Lol pV; Dactylis glomerata; Dac gV; epitope; sensitivity; ryegrass pollen allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
LPIX-2.1, peptide fragment of Lol pV protein allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 16;
8.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rice beta-glucanase gene Gns5 signal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 48; DB:
Pred. No. 8.7;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY09286 standard; Protein; 27 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 2; 110pp; English
                                                                                                                                                                                                                                                                                                                                 (IMMU-) IMMULOGIC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.5%;
64.3%;
                                                                                                                                                                                                                                             94WO-US09024.
                                                                                                                                                                                                                                                                                      93US-0106016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0050675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-US13525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 64.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                                                            Griffith IJ, Kuo M,
                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1995-115444/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 ATSPTAEGGKATTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 AA;
                                                                                                           Lolium perenne.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JUN-1997;
                                                                                                                                                                                                                                             05-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rodriguez RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JUN-1998;
                                                                                                                                                                                                                                                                                      13-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09859046-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-DEC-1998.
                                                                                                                                                      WO9506728-A.
                                                                                                                                                                                                 09-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY09286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
```

Rice;

RESULT

ŏ 셤 1;

Gaps

5;

ö

```
The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine. Cell proliferation or valid differentiations or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, o. stem cell growth factor activity, hemmatopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                  phi p bb, isolated from Graminae species. This allergen can be modified and the reactivity of the modified allergens with IgE antibodies to grass pollen allergens is reduced or eliminated while their reactivity with T cells is retained. The genes for the allergens are modified so that the encoded polypeptides have one or more amino acid substitutions, deletions and/or additions. The dominant T-cell epitopes of the allergens are not genetically altered. Such allergens have applications in the immunotherapy of allergies e.g. hyposensitisation.
                                                                                                                                                                                                                                                                                                                                      Gaps
                   AAW76449-W76534 are peptide fragments of a natural pollen allergen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID NO 17438; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                             DB 19; Length 12;
                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                      ;;
                                                                                                                                                                                                                                                                                           16.7%; Score 46; DB :
llarity 66.7%; Pred. No. 8.5;
Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human polypeptide SEQ ID NO 17438.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAO03546 standard; Protein; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-2001; 2001WO-US04927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                47
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-514838/56
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                36 QKLIEDVNASFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu C,
                                                                                                                                                                                                                                  12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAI83477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200164835-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT,
                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAO03546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAO03546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *00000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                            The present invention relates to novel plant transcription factors from Eucalyptus grandis or Pinus radiata. The present sequence is one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic hell's tipper. homeotic/homeodomain/homeobox/MADS, homeodomain cys2His2, CCAAT box elements and MYB.
                                                                                                                                                               New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pollen; allergen; Phl p 5b; IgE; antibody; grass; reactivity; T cell; epitope; immunotherapy; allergy; hyposensitisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified recombinant allergens - useful for immuno-therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 47; DB 21; Length 56;
Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Graminae pollen allergen Phl p 5b peptide fragment #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jaeger L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bufe A, Cromwell O, Flebig H, Mueller W, Schramm G, Stuewe H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                Glenn M;
                                         (FLET-) FLETCHER CHALLENGE FORESTS LTD.
                 (GENE-) GENESIS RES & DEV CORP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA.
                                                                                                                                                                                                                                                                         Claim 8; Page 742; 747pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 12; 31pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 PTAEGGKATTEEQKLIEDVNASF 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
                                                                                  Shenk MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW76457 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97DE-1013001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97DE-1013001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                McGrath A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-522170/45
                                                                                                                       WPI; 2000-579369/54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DE19713001-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kahlert H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Becker W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW76457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Graminae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                Wood M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW76457
```

qq

ò

8×3033

ò g

```
20000S - 0229344.
20000S - 0229344.
20000S - 0229344.
20000S - 0229513.
20000S - 0229513.
20000S - 0230437.
20000S - 0231244.
20000S - 0231243.
20000S - 0231244.
20000S - 0231244.
20000S - 0231244.
20000S - 0231244.
20000S - 0231298.
20000S - 0232398.
20000S - 0232399.
20000S - 0232409.
20000S - 0234274.
20000S - 0234274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20000S-0246525
20000S-0246525
20000S-0246526
20000S-0246528
20000S-0246528
20000S-0246632
20000S-0246609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0244617.
2000US-0246474.
2000US-0246475.
2000US-0246475.
2000US-0246477.
2000US-0246477.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0235834.
2000US-0235836.
2000US-0236327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0236368.
2000US-0236369.
2000US-0236370.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0237040.
2000US-0239935.
2000US-0239937.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0241221.
2000US-0241785.
2000US-0241786.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0241787.
2000US-0241808.
2000US-0241809.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0249207.
2000US-0249208.
2000US-0249209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0236802
2000US-0237037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0237038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0237039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0240960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0241826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0246611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0249210
2000US-0249211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0236367
 01-SEP-2000; 01-SEP-2000; 05-SEP-2000; 06-SEP-2000; 06-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-NOV-22000;
08-NOV-22000;
08-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
     ö
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.
                                                                                                                                                                             Gaps
                                                                                                                                                                           ;
                                                                                                                                 Score 45; DB 22; Length 33;
Pred. No. 44;
                                                                                                                                                                           6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immune/haematopoietic antigen SEQ ID NO:13269
                                                                                                                                                                         8; Mismatches
                                                                                                                                                                                                                                                                                                                                              AAM85676 standard; Protein; 57 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04 FEB. 2000; 20000S-018050.
04 FEB. 2000; 20000S-0184664.
02-MAR-2000; 20000S-0184664.
17-MAR-2000; 20000S-0189674.
18-APR-2000; 20000S-0199174.
19-MAY-2000; 20000S-0199173.
19-MAY-2000; 20000S-0199173.
19-MAY-2000; 20000S-0209467.
28-JUN-2000; 20000S-0214886.
30-JUN-2000; 20000S-0214886.
30-JUN-2000; 20000S-0214886.
30-JUN-2000; 20000S-0216880.
11-JUL-2000; 20000S-0217487.
11-JUL-2000; 20000S-0225787.
14-AUG-2000; 2000US-022577.
14-AUG-2000; 2000US-022577.
14-AUG-2000; 2000US-022577.
14-AUG-2000; 2000US-022577.
14-AUG-2000; 2000US-022577.
12-AUG-2000; 2000US-022577.
13-AUG-2000; 2000US-022577.
13-AUG-2000; 2000US-022577.
13-AUG-2000; 2000US-022577.
22-AUG-2000; 2000US-022577.
22-AUG-2000; 2000US-022577.
22-AUG-2000; 2000US-022577.
22-AUG-2000; 2000US-02277.
22-AUG-2000; 2000US-02277.
23-AUG-2000; 2000US-02277.
                                                                                                                                     16.4%;
26.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0179065.
2000US-0180628.
2000US-018664.
2000US-0186350.
2000US-0189874.
2000US-0199123.
2000US-0209467.
2000US-0209467.
2000US-0209467.
2000US-021686.
                                                                                                                                                                                                           1 MAAHKEMVAMFLAVAVVLG 19
: || |:: |::|
3 vtahafviiffivipiiig 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JAN-2001; 2001WO-US01354
                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                   Query Match 16.4
Best Local Similarity 26.3
Matches 5; Conservative
                                                                             33 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200157182-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                          07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                      AAM85676;
                                                                             Sequence
                                                                                                                                                                                                                                                                                                            14
                                                                                                                                                                                                                                                                                                                        AAM85676
                                                                                                                                                                                                                                                                                                            RESULT
```

Xenopus; activin receptor; human; c-myc tag; differentiation; neuron; transforming growth factor-beta; progenitor cell; neuralisation; activin; epidermis; embryonic morphogenesis; neural tissue; BMP; pluripotent; bone morphogenic protein; mouse; carcinoma; induction; epitope; wound; burn; tumour; artificial skin; cosmetic.

C-terminus of myc-tagged truncated Xenopus type II activin receptor.

(first entry)

04-JUN-1997

AAW07320;

24 AA.

AAW07320 standard; peptide;

/note- "C-terminus of truncated Xenopus type II activin receptor"

Location/Qualifiers

Region

Reg ton

Chimeric Xenopus sp. Chimeric Homo sapiens.

/note= "human c-myc tag"

WO9630038-A1

96WO-US04326.

29-MAR-1996; 29-MAR-1996; 29-MAR-1995;

03-OCT-1996

95US-0413047.

96US-0622860

```
AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
amino acid sequences given in AAM8110 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
cample, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
cample, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
cappelment the patients own production of (I). Additionally, (I)
polynucleotides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-derived cells. AAK64703
to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK84950 and AAM82169
represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and mersetacia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; SEQ ID NO 13269; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                        2000US-0251869
2000US-0251989
                                              2000US-0249215
                                                                                                 2000US-0249218
                                                                                                                                              2000US-0249264
                                                                                                                                                                                                                             2000US-0250160
                                                                                                                                                                                                                                                           2000US-0251030
                                                                                                                                                                                                                                                                            2000US-0251988
                                                                                                                                                                                                                                                                                          2000US-0256719
                                                                                                                                                                                                                                                                                                           2000US-0251479
                                                                                                                                                                                                                                                                                                                            2000US-0251856
                                                                                                                                                                                                                                                                                                                                          2000US-0251868
                                                                                                                                                                                                                                                                                                                                                                                       08-DEC-2000; 2000US-0251990
                                                                                                                                                                                                                                                                                                                                                                                                                       05-JAN-2001; 2001US-0259678
                                                                2000US-0249216
                                                                               2000US-0249217
                                                                                                              2000US-0249244
                                                                                                                                 2000US-0249245
                                                                                                                                                                2000US-0249265
                                                                                                                                                                             2000US-0249297
                                                                                                                                                                                              2000US-0249299
                                                                                                                                                                                                             2000US-0249300
                                                                                                                                                                                                                                            2000US-0250391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-483426/52.
N-PSDB; AAK58457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 AA;
                                                                                                                                                                                                                                                                          05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
                                                                                                                                           17 - NOV - 2000;
                                                                                                                                                                                                           17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
                                                                                                                                                                                                                                                                                                                                          08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                        08-DEC-2000;
                                              17-NOV-2000;
17-NOV-2000;
                                                                               17-NOV-2000;
                                                                                                                                                                                                                                                                                                                          08-DEC-2000;
                                                                                                             NOV-2000;
                                                                                                                               17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
```

Use of transforming growth factor-beta gene family prods. - for preventing or treating cellular debilitation(s), derangement(s) or dysfunction or other disease states.

P;

Hemmati-Brivanlou A, Wilson

(UYRQ ) UNIV ROCKEFELLER

Example 4; Page 49; 83pp; English.

```
3
                                   Gaps
                                     4
16.4%; Score 45; DB 22; Length 57; 32.4%; Pred. No. 89; ive 9; Mismatches 12; Indels
                                                                     22 TSPTAEGGKATTEEQKLIEDVNAS---FRAAMATTAN 55
                                                                                         Query Match 16.4
Best Local Similarity 32.4
Matches 12; Conservative
```

```
This sequence represents the C-terminal sequence of a truncated Xenopus type II activin receptor protein to which a human c-myc tag has been fused. The protein is used to study the role of transforming arouth factor (TGF) beta in the differentiation of progenitor cells into either neurons (neuralisation) or into epidermal cells during embryonic morphogenesis. This is based on the discovery that embryonic progenitor cells will automatically differentiate into neural tissue unless the cells are contacted with, or express, members of the TGF-beta family, such as activin or bone morphogenic protein (BMP)-4, whereupon the cells differentiate into epidermal tissue.

To study this effect in the P19 cell line, a pluripotent mouse embryonic carcinoma cell line, a dominant-negative truncated activin receptor from Xenopus was cloned into plasmid p286478 (see AAT42283) and transformed into P19 cells. The truncated receptor inhibits the induction of epidermis by the TGF-beta family protein. The truncated receptor is tagged with the myc epitope tag in order to identify the endogenous protein from the transformed protein. Induction of the formation of protein from the transformed protein. Induction of the formation of epidermis by the TGF-beta protein can be used for the treatment of e.g. which can be used for the testing of skin or cosmetics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 17; Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43; DB 1
Pred. No. 54;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
```

AAW07320 RESULT

g

ò

24 PTAEGGRATTEEQKLIED 41 | | | : |||| : 4 plqpggstssreqklise 21

Qy Dp

Search completed: July 11, 2002, 11:04:37 Job time: 214 sec

24, Appl . 5332671 . 5219739 51, Appl 15, Appl 15, Appl 15, Appl 15, Appl 15, Appl 15, Appl 26, Appl 26, Appl 27, Appl 28, Appl 2

Sequence Seq

Sequence Sequence

Sequence 1 Sequence 4 Sequence 2 Patent No. Patent No.

Perfect score:

ö

Scoring table: Sequence:

Database

```
Score 82; DB 1; Length 20;
Pred. No. 3.5e-05;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Griffith, Irwin J.
APPLICANT: Kuo, Mei-Chang
APPLICANT: Lugman, Mchammad
TITLE OF INVENTION: T CELL EPITOPES OF RYEGRASS POLLEN
TITLE OF INVENTION: ALLERGEN
                             US-08-440-861-4

US-09-105-390-24

5134596-21

5219739-26

US-08-779-113-51

US-08-433-864-15

US-08-174-745A-15

US-08-133-985-15

US-08-433-908-15

US-08-410-614-15

US-08-6117-121-16

US-09-117-121-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: IPC-075 (IMI-040cp)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,861
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
FILOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/106,016
FILING DATE: 31-AUG-1993
ATTONNEY/AGENT INFORMATION:
NAMME: AMNY E. MANGTAGOUTAS
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 5, Application US/08440861
; Patent No. 5710126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 29.8%;
Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 20 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-440-861-5
NUMBER OF SEQUENCES: 5:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-440-861-5
                                                                                                                                                                                                                                                 41
40
40
39.5
July 11, 2002, 11:02:53 ; Search time 12.87 Seconds (without alignments) 108.179 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17,
17,
17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7
                                                                                                                                                                                                                                               1 MAAHKFMVAMFLAVAVVLGL.....LIEDVNASFRAAMATTANVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_c/ptcdata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptcdata/2/iaa/5B_COMB.pep:*
/cgn2_e/ptcdata/2/iaa/6A_COMB.pep:*
/cgn2_e/ptcdata/2/iaa/6B_COMB.pep:*
/cgn2_e/ptcdata/2/iaa/PCTUS_COMB.pep:*
/cgn2_e/ptcdata/2/iaa/PCTUS_COMB.pep:*
             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-440-861-5
US-08-440-861-6
US-08-433-854-7
US-08-133-854-7
US-08-433-9088-7
US-08-433-9088-7
US-08-410-614-7
US-08-195-947-11
US-08-195-947-11
US-08-195-947-11
US-08-433-9088-11
US-08-433-9088-11
US-08-433-9088-11
US-08-433-9088-16
US-08-433-908-16
US-08-433-908-16
US-08-433-908-16
US-08-433-908-16
                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-174-745A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-195-947-17
US-08-433-885-17
                                                                                                                                                                                                                                                                                                                                               231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Issued_Patents_AA:*
                                                                                                                                                                                               US-09-696-169A-21
275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 57
```

Score

Result . 9 ö

Gaps

; 0

ò g

```
APPLICANT: Hough, Terryn
APPLICANT: Suphioglu, Cenk
APPLICANT: Suphioglu, Cenk
APPLICANT: Ong, Eng Kok
TITLE OF INVENTION: Ryegrass Pollen Allergen
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5736362ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
APPLICANT: Suphioglu, Cenk
APPLICANT: Ong, Eng Kok
TITLE OF INVENTION: Ryegrass Pollen Allergen
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STRREST: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 67; DB 1; Length 34; Pred. No. 0.009;
                                                                                                                                                                                                                                     ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,060
FILING DATE: 14-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: HOHORSCHULZ, LIZA D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: IMPH-0024
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir
APPLICANT: Knox, Robert B.
APPLICANT: Smith, Penelope
APPLICANT: Avjioglu, Asil
APPLICANT: Theerakulpisut, Piyada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08174745A Patent No. 5736362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.48;
72.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 ATSPTAEGGKATTEEOKL 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 72.2
Matches 13; Conservative,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: peptide US-08-433-854-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                         ΡA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-174-745A-7
                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                          CITY: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                  Sequence 6, Application US/08440861
| Patent No. 5710126
| GENERAL INFORMATION:
| APPLICANT: Kuo, Mei-Chang
| APPLICANT: Lugman, Mohammad
| TITLE OF INVENTION: ALCELL EPITOPES OF RYEGRASS POLLEN
| TITLE OF INVENTION: ALCELLE EPITOPES OF RYEGRASS POLLEN
| NUMBER OF SEQUENCES: 56
| CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: COCKFIELD
| STREET: 60 State Street, suite 510
| CITY: Boston
| STATE: Massachusetts
| COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 25.8%; Score 71; DB 1; Length 20; Best Local Similarity 70.0%; Pred. No. 0.0012; Matches 14; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,861
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/106,016
FILING DATE: 31-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: AMY E. MANDATAION:
REFERENCE/DOCKET NUMBER: 19C-075 (IMI-040CP)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-433-854-7

Sequence 7, Application US/08433854

Patent No. 5721119

GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir
APPLICANT: Smith, Penelope
APPLICANT: Smith, Penelope
APPLICANT: Avjioglu, Asil
APPLICANT: Theerakulpisut, Piyada
APPLICANT: Hough, Terryn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EQKLLEDVNAGFKAAVAAAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35 EQKLIEDVNASFRAAMATTA 54
                                                  2 AAGGKATTDEQKLLEDVNA 20
                         26 AEGGKATTEEQKLIEDVNA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02109
                                                                                                                                                                       US-08-440-861-6
```

q

```
24.48;
72.28;
   (215) 568-3100
                   TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                   21 ATSPTAEGGKATTEEQKL 38
                                                                                                                                                                                                                                                                                                                      17 AATPAAAGGKATTDEQKL 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 ATSPTAEGGKATTEEQKL 38
                                                                           LENGTH: 34 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 34 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                              13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-195-947-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: peptide US-08-433-885-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boston
 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
US-08-433-885-7
                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5840316ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 67; DB 1; Length 34; Pred. No. 0.009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 14-FEB-1994
CLASSIFICATION: 435
               SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/174,745A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hough, Terryn
APPLICANT: Suphioglu, Cenk
APPLICANT: Ong, Eng Kok
TITLE OF INVENTION: Ryegrass Pollen Allergen
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,060
FILING DATE: 14-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: HOHENSCHUZ, LIZA D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: IMPH-0024
TELECOMUNICATION INFORMATION:
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMPH-0024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,060
FILING DATE: 14-AUG-1992
ATTORNEY-AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Singh, Mohan Bir
Knox, Robert B.
Smith, Penelope
Avjioglu, Asil
Theerakulpisut, Piyada
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08195947
Patent No. 5840316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: IME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 ATSPIAEGGKATTEEQKL 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | :| | ||||||:||||
|17 AATPAAAGGKATTDEQKL 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Conservative
                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-174-745A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TAPPLICANT:
APPLICANT:
APPLICANT:
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-08-195-947-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                               Gaps
                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
  Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,885
FILING DATE: 02-MAY-1995
CLASSIFICATION: 435
Score 67; DB 2;
Pred. No. 0.009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 67; DB 2;
Pred. No. 0.009;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hough, Terryn
APPLICANT: Suphioglu, Cenk
APPLICANT: Ong, Eng Kok
TITLE OF INVENTION: Ryegrass Pollen Allergen
NUMBER OF SEQUENCES: 53
                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: IMI-039C2D2 TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 227-7400 TELEPAX: (617) 227-5941 INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Lahive & Cockfield
60 State Street, Suite 510
                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir
APPLICANT: Knox, Robert B.
APPLICANT: Smith, Penelope
APPLICANT: Avjioglu, Asil
APPLICANT: Theerakulpisut, Piyada
                                                                                                                                                                                                                                          ; Sequence 7, Application US/08433885
; Patent No. 5869333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Any E.
REGISTRATION NUMBER: 36,207
```

g

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5721119ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 6277383ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                     COUNTRY: USA
ZIE: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Singh, Mohan Bir
APPLICANT: Singh, Mohan Bir
APPLICANT: Singh, Penelope
APPLICANT: Avjioglu, Asil
APPLICANT: Theerakulpisut, Piyada
APPLICANT: Hough, Terryn
APPLICANT: Suphioglu, Cenk
APPLICANT: Suph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 67; DB 4;
Pred. No. 0.009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/195,947
FILING DATE: 14 FEB-1994
APPLICATION NUMBER: US 07/930,060
FILING DATE: 14 ANG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: IMPH-0024
TELECOMMUNICATION INFORMATION:
TELEFHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-433-854-11; Sequence 11, Application US/08433854; Patent No. 5721119; Patent INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.48;
72.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 ATSPTAEGGKATTEEQKL 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 24.4
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: peptide US-08-410-614-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΡA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: F
                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-FOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,908B
FILING DATE: 0.2-MAY-1995
                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir
APPLICANT: Singh, Mohan Bir
APPLICANT: Smith, Penelope
APPLICANT: Avjioglu, Asil
APPLICANT: Theerakulpisut, Piyada
APPLICANT: Hough, Terryn
APPLICANT: Gug, Eng Kok
TITLE OF INVENTION: Ryegrass Pollen Allergen
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 67; DB 2;
Pred. No. 0.009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hough, Terryn
APPLICANT: Suphioglu, Cenk
APPLICANT: Ong, Eng Kok
TITLE OF INVENTION: Ryegrass Pollen Allergen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Mandraguras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 1MI-039C2D4
TELECOMMUNICATION INFORMATION:
TELECHONE: (617) 227-7400
TELETAX: (617) 242-414
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Lahive & Cockfield, LLP STREET: 28 State Street CITY: Boston STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/08410614
Patent No. 6277383
GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir
APPLICANT: Singh, Penelope
APPLICANT: Smith, Penelope
SAPLICANT: Apjoglu, Asil
APPLICANT: Theerakulpisut, Plyada
                                                                                                                                                       Sequence 7, Application US/08433908B Patent No. 5965455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 ATSPTAEGGKATTEEQKL 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | :| | |||||||:|||||
17 AATPAAAGGKATTDEQKL 34
   17 AATPAAAGGKATTDEQKL 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 72.2'
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 34 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: peptide US-08-433-908B-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
US-08-410-614-7
```

g ò

us-09-696-169a-21.closed.rai

ŏ g

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6277383ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 66; DB 2; Length 21;
Pred. No. 0.0066;
1; Mismatches 2; Indels
                                                                                                                                                                                        COUNTRY: USAN 21P: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,908B
FILING DATE: 02-MAY-1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: MANDARAGOUTAS, AMY E.
REGISTRATION NUMBER: IMI-039C2D4
TELEPROCKET NUMBER: IMI-039C2D4
TELEPROMONICATION INFORMATION:
TELEPRONE (617) 722-7400
TELEFAX: (617) 722-7410
TELEPRATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
FWATH. 21 AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/08410614
Fatent No. 6277383
GENERAL INFORMATION:
APPLICANT: Sligh, Mohan Bir
APPLICANT: Snith, Penelope
APPLICANT: Smith, Penelope
APPLICANT: Theerakulpisut, Plyada
APPLICANT: Theerakulpisut, Piyada
APPLICANT: Hough, Terryn
APPLICANT: Wolf, Terryn
APPLICANT: Ong, Eng Kok
TITLE OF INVENTION: Ryegrass Pollen Allergen
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
    APPLICANT: Ong, Eng Kok
TITLE OF INVENTION: Ryegrass Pollen Allergen
                                            NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSE: Lahive & Cockfield, LLP
STREET: 28 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 24.0
Best Local Similarity 81.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 SPTAEGGKATTEEQKL 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-433-908B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-410-614-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 66; DB 2; Length 21;
Pred. No. 0.0066;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC COMPAtible
OPRAPING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/43,885
FILING DATE: O2-MAY-1995
ATTONNEY/AGNET INFORMATION:
AMAGINET INFORMATION:
NAME: MANDERMATION:
REGISTRATION NUMBER: 36,207
REFERENCE/POCKET UNMBER: 36,207
REFERENCE/COCKET UNMBER: 36,207
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELEFRAX: (617) 227-7400
TELEFRAX: (617) 227-7400
TELEFRAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
TENGTH. 21 amino acids
                                                                                                                                                  Sequence 11, Application US/08433885
Patent No. 5869333
GENERAL INFORMATION:
APPLICANT: Singh Mohan Bir
APPLICANT: Snith, Penelope
APPLICANT: Avjoqlu, Asil
APPLICANT: Theerakulpisut, Piyada
APPLICANT: Hough, Terryn
APPLICANT: Hough, Terryn
APPLICANT: Hough, Terryn
APPLICANT: Ong, Bng Kok
TITLE OF INVENTION: Ryegrass Pollen Allergen
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Lahive & Cockfield
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/08433908B; Patent No. 5965455; GENERAL INFORMATION: APPLICANT: Singh, Mohan Bir APPLICANT: Singh, Mohan Bir APPLICANT: Smith, Penelope APPLICANT: Theerakulpisut, Piyada APPLICANT: Heerakulpisut, Piyada APPLICANT: Hough, Terryn APPLICANT: Suphioglu, Cenk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.0%;
81.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match ' 24.0
Best Local Similarity 81.2
Matches 13; Conservative
23 SPTAEGGKATTEEQKL 38
                         23 SPTAEGGKATTEEOKL 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-433-908B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                    US-08-433-885-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-433-885-11
```

ò qq

Gaps

ö

```
ADDRESSEE: Woodcock Washburn Kurtz Macklewicz 6 No. 5840316ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                        Score 66; DB 1; Length 21;
Pred. No. 0.0066;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.0%; Score 66; DB 2; Length 21; 81.2%; Pred. No. 0.0066; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,947
FILING DATE: 14-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION ATA:
APPLICATION WHERE: US/08/195,947
FILING DATE: 14-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION THEORMATION:
APPLICATION NUMBER: US/930,060
FILING DATE: 14-AUG-1992
ATORNEY/AGENT INFORMATION:
NAME: HOHORSCHULZ, LIZA D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: IMPH-0024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Singh, Mohan Bir
APPLICANT: Singh, Pobert B.
APPLICANT: Smith, Penelope
APPLICANT: Avjioglu, Asil
APPLICANT: Hough, Terryn
APPLICANT: Suphioglu, Cenk
APPLICANT: Suphioglu, Cenk
APPLICANT: Ong, Eng Kok
TITLE OF INVENTION: Ryegrass Pollen Allergen
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/08195947 Patent No. 5840316 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          24.0%;
81.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
  (215) 568-3439
                                                                  : LENGTH: 21 amino acids

: TYPE: amino acid

: TOPOLOGY: linear

: MOLECULE TYPE: peptide

US-08-174-745A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 21 amino acids
amino acid
                                                                                                                                                                                                                   Query Match
Best Local Similarity 81.2
Matches 13; Conservative
                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 24.0
Best Local Similarity 81.2
Matches 13; Conservative
                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                 23 SPTAEGGKATTEEQKL 38
                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: peptide US-08-195-947-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-195-947-11
    TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Singh, Mohan Bir
APPLICANT: Singh, Mohan Bir
APPLICANT: Singh, Penelope
APPLICANT: Suith, Penelope
APPLICANT: Avijoglu, Arijoglu, Peresakulpisut, Piyada
APPLICANT: Theerakulpisut, Piyada
APPLICANT: Suphioglu, Cenk
APPLICANT: Suphioglu, Cenk
APPLICANT: Ong, Eng Kok
TITLE OF INVENTION: Ryegrass Pollen Allergen
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 5736362ris
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 66; DB 1; Length 21;
Pred. No. 0.0066;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/174,745A
FILING DATE:
PatentIn Release #1.0, Version #1.25
                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,060
FILING DATE: 14.ACG-11992
ATTORNEY/AGENT INFORMATION:
NAME: HOHENSCHUTZ, LIZA D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: IMPH-0024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Hohenschutz, Liza D. REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: IMPH-0024
TELECOMMUNICATION:
TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,060
FILING DATE: 14 - MUG-1992
ATTORNEY/AGENT INFORMATION:
                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11; Application US/08174745A Patent No. 5736362 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      relephone: (215) 568-3100
TELERX: (215) 568-349
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acids
TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.0%;
81.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 81.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 SPTAEGGKATTEEQKL 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: peptide US-08-433-854-11
                                                                                      CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Philadelphia
                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-174-745A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Пр
```

ô

```
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                 οy
                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FALCEL NO. CALLED

APPLICANT: Griffith, Irwin J.
APPLICANT: Griffith, Irwin J.
APPLICANT: Kuo, Mei-Chang
APPLICANT: Lugman, Mohammad

TITLE OF INVENTION: T CELL EPITOPES OF RYEGRASS POLLEN
TITLE OF INVENTION: ALLERGEN

NUMBER OF SQUENCES: 56
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 66; DB 4; Length 21;
Pred. No. 0.0066;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Any E. Mandragouras
NAME: Any E. Mandragouras
REGISTRATION NUMBER: 36,207
REPORMICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
          PRIOR APPLICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NDATA:
PRIOR APPLICATION NUMBER: US 08/195,947
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 07/930,060
FILING DATE: 14-MC-1992
ATTORNEY/AGENT INFORMATION:
NAME: HOADSCHULZ, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: IMPH-0024
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INCOMMATION:
TELECOMUNICATION INCOMMATION:
SEQUENCE CHARACTERISTICS:
LENGTH 21 and no acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 'IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,861
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION HAR:
APPLICATION NUMBER: US 08/106,016
FILING DATE: 31-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 54, Application US/08440861
Patent No. 5710126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match ' 24.0
Best Local Similarity 81.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 SPTAEGGKATTEEOKL 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-410-614-11
                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-440-861-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
MOLECULE TYPE: peptide

FEATURE: FEATURE: N-terminal
FEATURE: N-terminal
MAME/KEY: misc_feature

LOCATION: 7, 13, 16, 20,
CTHER INFORMATION: /label-Pro is 4Hyp
US-08-440-861-54

Query Match
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps

Qy 21 ATSPTAEGGKATTEEQK 37

| | | | | | | | | | | | |
Db 17 AATPAAGGKATTDEQK 33

Search completed: July 11, 2002, 11:04:56
Job time: 123 sec
```

Graminae pollen al Graminae pollen al LPIX-8, peptide fr MAD anti-HBSAG bin Integrin alpha-6a Drosophila melanog Peptide #1171 enco Peptide #1211 enco

Human bone marrow Peptide #1174 enco Peptide #1200 enco Peptide #1144 enco

Human secreted pro Graminae pollen al Human immune/haema Novel human diagno

Human brain expres

pro

Staphylococcus aur Human secreted pro

Drosophila melanog

Kentucky Blue Gras Cationic peptide a

Cationic peptide A

gene a

coli AMP

Physcomitrella pat

Peptide #9114 enco

Graminae pollen al LPIX-5, peptide fr

Amino acid residue Graminae pollen al Insulin 1 B-chain.

LPIX-6, peptide fr

Perfect score:

Sequence:

OM protein

o o

Run

Scoring table:

Searched:

Minimum DB Maximum DB

Database

```
Major histocompatibility complex; class II; desensitising; human; allergen; grass; tree; weed; pollen; fungi; mould; food; insect; sting; chiromidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybbe; screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat; cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig; mice; gerbll; vaccine; treatment; prevention; hypersensitivity.
                                                                                                                                                                                                                                                                  Phleum sp. allergen Phl p 6 protein fragment #2
                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                 (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
                                                                                           AAM91429
AAR71513
ABG27510
AAY42432
AAW76486
                                                                                                                                                              AAW66394
AAY91693
AAB51195
    AAW76485
AAR71515
AAW10845
AAW10860
AAR80961
ABB70488
                                                     AAM54473
AAM66878
AAM14740
AAM27163
AAM02462
AAY41313
                                                                                                                            AAW79410
AAB32429
ABB67490
AAW76484
                                           ABB33705
ABB19154
                                                                                                                                                   AAR71512
AAR89394
                                                                                                                        AAW47366
                                                                                                                                                                               AAB99854
                                                                                                                                                                                                                                 AAY25637 standard; protein; 57 AA
98GB-0000445
                                                                                                                                                                                                                                                                                                                                                     99WO-GB00080
                                                                                                                                                                                                                                                                                                                                                                98GB-0020474
                                                                                                                                                                                                                                                       30-SEP-1999 (first entry)
WPI; 1999-458255/38
                                                                                                                                                                                                                                                                                                                                                                                            Larche M;
W09934826-A1
                                                                                                                                                                                                                                                                                                                                                     11-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                      09-JAN-1998;
                                                                                                                                                                                                                                                                                                                                           15-JUL-1999
Phleum sp
                                                                                                                                                                                                                                                                                                                                                                                            Kay AB,
                                                                                                                                                                                                                           AAY25637
RESULT
                                                                                                                                                                                                                                      Phleum sp. allerge
Kentucky Blue Gras
LPIX-10, peptide f
LPIX-9, peptide f
LPIX-11, peptide f
LPIX-12, peptide f
Kentucky Blue Gras
LPIX-13, peptide f
Kentucky Blue Gras
Graminae pollen al
C glutamicum prote
                                                                                                                                                                 July 11, 2002, 10:52:12; Search time 29.77 Seconds (without alignments) 212.671 Million cell updates/sec
                                                                                                                                                                                                                                                                                                   number of results predicted by chance to have a an or equal to the score of the result being printed, y analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                           Description
                                                                      1 SKAPQLVPKLDEVYNAAYNA.....SEALHIIAGTPEVHAVKPGA
    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                 747574 seqs, 111073796 residues
                          - protein search, using sw model
                                                                                                                                                    Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                    AAY25637
AAR89393
AAR71517
AAR71516
AAR71519
AAR89392
AAR89392
AAR89391
AAR89391
AAR89391
                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                         score greater than or equal to and is derived by analysis of
                                                                                                                                       Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                              A_Geneseq_032802:*
                                                         US-09-696-169A-19
297
                                                                                                                                                                                                                                                                                                                                                     20
110
110
110
110
110
                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                     57
20
20
20
20
20
20
20
53
                                                                                                                       seq length: 0 seq length: 57
                                                                                                                                                                                                                                                                                                   the
                                                                                                                                                                                                                                                                                                                                    Query
Match 1
                                                                                                                                                                                                                                                                                                                                                     15.2
15.2
15.2
                                                                                                                                                                                                               ţ,
```

ŞO.

Pred.

Result Š 297 707 65 65 54 74 74 74 75

110 98 7 110

```
Lolium perenne.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                    02-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9506728-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-MAR-1995.
                                                                                                                                                                                                                                                                                                                                                          AAR71517;
                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                         m
                                                                                                                                                                                                                                                                                                        RESULT
AAR71517
  888888888888888
                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel method of desensitizing a patient to a polypeptide allergen and comprises administering to the patient a peptide derived from the allergen where restriction to a MHC Class II molecule possessed by the patient can be demonstrated for the peptide and the peptide is able to induce a late phase response in an individual who spessesses the MHC class II molecule. The methods can be used for desensitising patients to allergens present in e.g. grass, tree and weed (including ragweed) pollens, fungi and moulds, foods, stinging insects, the chiromidae (non-biting midges), spiders and mites, housefly, fruit fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee, non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of Tenibric molitor beetle, mammals such as cat, dog, horse, cow, pig, sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to produce immunological vaccines which may be used to prevent and/or treat
                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide including at least 1 human antigenic determinant of Kentucky Blue Grass allergen - from Poo p IX 9p. of grass polien allergens, used to desensities allergic individuals, prevent grass pollen allergy and deplete allergen-specific antibodies
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present peptide is a human antigenic determinant contg. peptide,
                                                                                                                                                                                                                                                                                                                                                                                     1 SKAPQLVPKLDEVYNAAYNAADHAAPEDKYEAFVLHFSEALHIIAGTPEVHAVKPGA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antigenic determinant; recombinant; Kentucky Blue Grass; pollen; allargeni; artigenic; r8B660; Poa p IX group; desensitisation; allargi; allargy; prevention; development; reaction; grass; antibody; anergise; producing cell; diagnosis; human; clone 60;
                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                  Length 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kentucky Blúe Grass pollen allergen rKBG60 resides 129-148.
                                                                                                                                                                                                                                                    represents a Phleum sp. (Timothy grass) Phl p 6 allergen.
                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunological response; B-cell; higG; higE; T-cell
                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                    DB 20;
                                                                                                                                                                                                                                                                                                                  100.0%; Score 297; DB 20;
100.0%; Pred. No. 2.6e-32;
iive 0; Mismatches 0;
 Desensitizing patients to polypeptide allergens
                         Example 6; Page 65; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 5; Page 29; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR89393 standard; peptide; 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94US-0280455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95WO-CA00439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-SEP-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                            57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYMA-) UNIV MANITOBA.
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-116753/12.
                                                                                                                                                                                                                                                                              57 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pratensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9603106-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mohapatra SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-FEB-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR89393;
                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Poa
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR89393
ó
                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lol pV, is a major allergen of ryegrass pollen, and is encoded by the CDNA sequence of clone 12R (AAQ85932), a full-length clone derived from a lambda gill library. Peptides (AAR71508-61) comprising at least one T cell epitope derived from the Lol pV protein are claimed, and can be used to treat or diagnose sensitivity to ryegrass pollen in an individual or to pollen proteins that are immunologically related to Lol pV, such as Dac gV (see AAR71507).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
comprising residues 129-148 of the recombinant Kentucky Blue Grass pollen allergen rKBG60, which is from the Poa p IX gp. of grass pollen allergens. A compsn. comprising the peptide and a carrier can be used to desensitise allergic individuals, and prevent allergic individuals from developing an allergic reaction to grass pollen. The compsn. may also be used to deplete allergen specific antibodies from an individual, and anergise allergen specific antibody producing cells. The peptide can be used to diagnose grass pollen allergy, and has the following human immunological response profile, B-cell (hIgG (-)/hIgE (-)), T-cell (-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lolium perenne Lol pV and Dactylis glomerata Dac gV epitope(s) and DNA - for treating sensitivity to rye-grass pollen allergen or an immunologically cross-reactive allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lolium perenne; Lol pV; Dactylis glomerata; Dac gV; epitope; sensitivity; ryegrass pollen allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 70; DB 17; Length 20; Pred. No. 0.016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 65; DB 16; Length 20; Pred. No. 0.076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LPIX-10, peptide fragment of Lol pV protein allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR71517 standard; Protein; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Luqman M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 2; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IMMU-) IMMULOGIC PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                          23.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94WO-US09024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 SEALHIIAGTPEVHAVKP 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||| ||||| |||| ||| ||| 2 sealrijagtlevhgvkp 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Griffith IJ, Kuo M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-115444/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 15; Conser
                                                                                                                                                                                                                                                                                                                                               20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 AA;
```

```
Lolium perenne Lol pV and Dactylis glomerata Dac gV epitope(s) and DNA - for treating sensitivity to rye-grass pollen allergen or an immunologically cross-reactive allergen.
                                                                                                                                                                                                           Claim 1; Fig 2; 110pp; English.
                                                                                                      (IMMU-) IMMULOGIC PHARM CORP
                                                                                  93US-0106016.
                                                               94WO-US09024
                                                                                                                            Kuo M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kuo M,
                                                                                                                                               WPI; 1995-115444/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-115444/15.
                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                20 AA;
   Lolium perenne.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lolium perenne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Griffith IJ,
                                                                                                                           Griffith IJ,
                                                             05-AUG-1994;
                                                                                  13-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-NOV-1995
                     WO9506728-A
                                         09-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9506728-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-MAR-1995.
                                                                                                                                                                                                                                                                                                                  Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR71519;
                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR71519
  δ
                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                Lol pV, is a major allergen of ryegrass pollen, and is encoded by the CDNA sequence of clone 12R (AAQ85932), a full-length clone derived from a lambda gtll library. Peptides (AAR71508-61) comprising at least one T cell epitope derived from the Lol pV protein are claimed, and can be used to treat or diagnose sensitivity to ryegrass pollen in an individual or to pollen proteins that are immunologically related to Lol pV, such as Dac gV (see AAR71507).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                    Lolium perenne Lol pV and Dactylis glomerata Dac gV epitope(s) and DNA - for treating sensitivity to rye-grass pollen allergen or an immunologically cross-reactive allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                       Lolium perenne; Lol pV; Dactylis glomerata; Dac gV; epitope; sensitivity; ryegrass pollen allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lolium perenne; Lol pV; Dactylis glomerata; Dac gV; epitope; sensitivity; ryegrass pollen allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPIX-11, peptide fragment of Lol pv protein allergen.
                                                                                                                                   LPIX-9, peptide fragment of Lol pv protein allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 62; DB
Pred. No. 0.19
3; Mismatches
                                                                      AAR71516 standard; Protein; 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR71518 standard; Protein; 20 AA.
                                                                                                                                                                                                                                                                                                                Luqman M;
                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 2; 110pp; English
 33
          |: || ||: | || ||: ||
1 ydvaykaaegatpeakydaf 20
                                                                                                                                                                                                                                                                                          (IMMU-) IMMULOGIC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.9%;
                                                                                                                                                                                                                                                                       93US-0106016.
                                                                                                                                                                                                                                                  94WO-US09024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | |:|||| |: || ||:
| pglipkldtaydvaykaae 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PQLVPKLDEVYNAAYNAAD 22
                                                                                                               (first entry)
14 · YNAAYNAADHAAPEDKYEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 20.9
Best Local Similarity 57.9
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                               Kuo M,
                                                                                                                                                                                                                                                                                                                                  WPI; 1995-115444/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 AA;
                                                                                                                                                                                      Lolium perenne.
                                                                                                                                                                                                                                                                                                              Griffith IJ)
                                                                                                                                                                                                                                                  05-AUG-1994;
                                                                                                                                                                                                                                                                       13-AUG-1993;
                                                                                                               02-NOV-1995
                                                                                                                                                                                                          W09506728-A
                                                                                                                                                                                                                             09-MAR-1995.
                                                                                          AAR71516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR71518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ŋ
                                                            AAR71516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
```

```
Lol pV, is a major allergen of ryegrass pollen, and is encoded by the CDNA sequence of clone 12R (AAQ85932), a full-length clone derived from a lambda gtll library. Peptides (AAR71508-61) comprising at least one T cell epitope derived from the Lol pV protein are claimed, and can be used to treat or diagnose sensitivity to ryegrass pollen in an individual or to pollen proteins that are immunologically related to Lol pV, such as Dac gV (see AAR71507).
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lolium perenne Lol pV and Dactylis glomerata Dac gV epitope(s) and DNA - for treating sensitivity to rye-grass pollen allergen
                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lollum perenne; Lol pV; Dactylis glomerata; Dac gV; epitope; sensitivity; ryegrass pollen allergen.
                                                                                                                                                                                                                                                                                                                                             Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPIX-12, peptide fragment of Lol pV protein allergen.
                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                          18.9%; Score 56; DB 16; 55.0%; Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR71519 standard; Protein; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Luqman M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 AAPEDKYEAFVLHFSEALHI 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | || || || :||| :||| :||| 1 atpeakydafvtaltealrv 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IMMU-) IMMULOGIC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93US-0106016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94WO-US09024.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
```

4

ö

Gaps

ö

```
Lol pV, is a major allergen of ryegrass pollen, and is encoded by the CDNA sequence of clone 12R (AAQ85932), a full-length clone derived from a lambda gill library. Peptides (AAR71508-61) comprising at least one T cell epitope derived from the Lol pV protein are claimed, and can be used to treat or diagnose sensitivity to ryegrass pollen in an individual or to pollen proteins that are immunologically related to Lol pV, such as Dac gV (see AAR71507).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lolium perenne Lol pV and Dactylis glomerata Dac gV epitope(s) and DNA - for treating sensitivity to rye-grass pollen allergen or an immunologically cross-reactive allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lolium perenne; Lol pV; Dactylis glomerata; Dac gV; epitope; sensitivity; ryegrass pollen allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 16; Length 20;
                                                                                                                         17; Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPIX-13, peptide fragment of Lol pV protein allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                      5,
profile, B-cell (higG (-)/higE (-)), T-cell (+).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 14;
0; Mismatches
                                                                                                                         DB
                                                                                                                                                  Pred. No. 11;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48;
Pred. No. 1
                                                                                                                         Score 49;
                                                                                                                                                                                                                                                                                                                                                                                             AAR71520 standard; Protein; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR89391 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 2; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lugman M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.2%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IMMU-) IMMULOGIC PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93US-0106016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94WO-US09024
                                                                                                                      16.5%;
50.0%;
                                                                                                                                                                                                                                                  17 AYNAADHAAPEDKYEAFV 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                      Query Match 16.5
Best Local Similarity 50.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Griffith IJ, Kuo M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 IAGTPEVHAVKP 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||| ||||||||
| iagalevhavkp 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1995-115444/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 AA;
                                                20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lolium perenne.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9506728-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR71520;
                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         σ
                                                                                                                                                                                                                                                                                                                                             ω
                                                                                                                                                                                                                                                                                                                                                                         AAR71520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR89391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΩX
  S X C
                                                                                                                                                                                                                         δy
                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                     Lol pV, is a major allergen of ryegrass pollen, and is encoded by the cDNA sequence of clone 12R (AAQ85932), a full-length clone derived from a lambda gtll library. Peptides (AAR71508-61) comprising at least one T cell epitope derived from the Lol pV protein are claimed, and can be used to treat or diagnose sensitivity to ryegrass pollen in an individual or to pollen proteins that are immunologically related to Lol pV, such as Dac gV (see AAR71507).
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide including at least 1 human antigenic determinant of Kentucky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present peptide is a human antigenic determinant contg. peptide, comprising residues 109-128 of the recombinant Kentucky Blue Grass pollen allergen rKBG60, which is from the Poa p IX 9p. of grass pollen allergens. A compson. comprising the peptide and a carrier can be used to desensitise allergic individuals, and prevent allergic individuals from developing an allergic reaction to grass pollen. The compson may also be used to deplete allergen specific antibodies from an individual, and anergise allergen specific antibody producing cells. The peptide can be used to diagnose grass pollen allergy, and has the following human immunological response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blue Grass allergen - from Poa p IX gp. of grass pollen allergens, used to desensitise allergic individuals, prevent grass pollen allergy and deplete allergen-specific antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigenic determinant; recombinant; Kentucky Blue Grass; pollen; allergen; antigenic; rKBG60; Poa p IX group; desensitisation; allergi; prevention; development; reaction; grass; antibody; anergise; producing cell; diagnosis; human; clone 60; immunological response; B-cell; hIgG; hIgE; T-cell.
                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kentucky Blue Grass pollen allergen rKBG60 resides 109-128.
                                                                                                                                                                                                                                                                                                                                                                    18.2%; Score 54; DB 16; Length 20; 60.0%; Pred. No. 2.3; cive 2; Mismatches 6; Indels
or an immunologically cross-reactive allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR89392 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Page 29; 59pp; English.
                                                Claim 1; Fig 2; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95WO-CA00439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94US-0280455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 VLHFSEALHIIAGTPEVHAV
                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 60.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYMA-) UNIV MANITOBA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-116753/12.
                                                                                                                                                                                                                                                                                             20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pratensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mohapatra SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9603106-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-FEB-1996,
                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR89392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Poa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR89392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A STATE OF S
ò
```

ö

Gaps

Ľ,

```
AAW76449-W76534 are peptide fragments of a natural pollen allergen, phl p 5b, isolated from Graminae species. This allergen can be modified and the reactivity of the modified allergens with IgE antibodies to grass pollen allergens is reduced or eliminated while their reactivity with T cells is retained. The genes for the allergens are modified so that the encoded polypeptides have one or more amino acid substitutions, deletions and/or additions. The dominant T-cell epitopes of the allergens are not genetically altered. Such allergens have applications in the immunotherapy of allergies e.g. hyposensitisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                   Modified recombinant allergens - useful for immuno-therapy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 19; Length 12;
19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashi M, Ochiai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C glutamicum protein fragment SEQ ID NO: 6796.
                                                                                                                                                                                                       Fiebig H,
Stuewe H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mizoguchi H, Ando S, Hayas
Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.2%; Score 45;
81.8%; Pred. No. 1
                                                                                                                                                                                                       Bufe A, Cromwell O, F
Mueller W, Schramm G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG93042 standard; Protein; 53 AA.
                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 12; 31pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                             97DE-1013001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000JP-0159162.
2000JP-0280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99JP-0377484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-DEC-2000; 2000EP-0127688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-SEP-2001 (first entry)
                                                                                                                                                                  (MERE ) MERCK PATENT GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organic acid synthesis.
                                                                                                                                                                                                                                                              WPI; 1998-522170/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SKAPQLVPKLD 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :||| ||||||
| akapglvpkld 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                   DE19713001-A1
                                                                                       27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP1108790-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-DEC-1999;
                                                        01-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nakagawa S,
Tateishi N,
                                                                                                                                                                                                                         Kahlert H,
                                                                                                                                                                                                         3
                                                                                                                                                                                                                                                                                                                        allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG93042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1
δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pollen; allergen; Phl p 5b; IgE; antibody; grass; reactivity; T cell; epitope; immunotherapy; allergy; hyposensitisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide including at least 1 human antigenic determinant of Kentucky Blue Grass allergen - from Poa p IX gp. of grass pollen allergens, used to desensitise allergic individuals, prevent grass pollen allergy and deplete allergen-specific antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present peptide is a human antigenic determinant contg. peptide, comprising residues 99-118 of the recombinant Kentucky Blue Grass pollen allergen rKBG60, which is from the Poa p IX gp. of grass pollen allergens. A compson. comprising the peptide and a carrier can be used to desensitise allergic individuals, and prevent allergic individuals from developing an allergic reaction to grass pollen. The compson may also be used to deplete allergen specific antibody producing cells. The peptide can be used to diagnose grass pollen allergy, and has the following human immunological response profile, B-cell (higg (-)/higE (+)), T-cell (+).
                                                                                                      Antigenic determinant; recombinant; Kentucky Blue Grass; pollen; allergen; antigenic; rKBG60; Poa p IX group; desensitisation; allergic; allergy; prevention; development; reaction; grass; antibody; ahergise; producting cell; diagnosis; human; clone 60; immunological response; B-cell; hIgG; hIgE; T-cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .<u>`</u>
                                                                   Kentucky Blue Grass pollen allergen rKBG60 resides 99-118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Graminae pollen allergen Phl p 5b peptide fragment #23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 47; DB 17;
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Page 29; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW76471 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.8%;
50.0%;
                                                                                                                                                                                                                                                                                                                                   95WO-CA00439
                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 kldaayklayksaegatp 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 50.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 KLDEVYNAAYNAADHAAP
                                                                                                                                                                                                                                                                                                                                                                                                             (UYMA-) UNIV MANITOBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-116753/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 AA;
                                                                                                                                                                                                                         Poa pratensis
                             17-SEP-1996
                                                                                                                                                                                                                                                          WO9603106-A2
                                                                                                                                                                                                                                                                                                                                   26-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mohapatra SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-DEC-1998
                                                                                                                                                                                                                                                                                             08-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW76471;
```

ö

Gaps

ö

1; Indels

Yokoi H;

Graminae

RESULT

쉽 ð

Gaps

ö

Indels

. ن

```
AAW76449-W76534 are peptide fragments of a natural pollen allergen, Phl p 5b, isolated from Graminae species. This allergen can be modified and the reactivity of the modified allergens with igg antibodies to grass pollen allergens is reduced or eliminated while their reactivity with T cells is retained. The genes for the allergens are modified so that the encoded polypeptides have one or more amino acid substitutions, deletions and/or additions. The dominant T-cell epitopes of the allergens are not genetically altered. Such allergens have applications in the immunotherapy of allergies e.g. hyposensitisation.
 and the reactivity of the modified allergens with IgE antibodies to grass pollen allergens is reduced or eliminated while their reactivity with T cells is retained. The genes for the allergens are modified so that the encoded polypeptides have one or more amino acid substitutions, deletions and/or additions. The dominant T-cell epitopes of the allergens are not genetically altered. Such allergens have applications in the immunotherapy of allergies e.g. hyposensitisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pollen; allergen; Phl p 5b; IgE; antibody; grass; reactivity; T cell; epitope; immunotherapy; allergy; hyposensitisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified recombinant allergens - useful for immuno-therapy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44; DB 19; Length 12; Pred. No. 26;
                                                                                                                                                                                    DB 19; Length 12; 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Graminae pollen allergen Phl p 5b peptide fragment #37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fiebig H, Stuewe H;
                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                      Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                     AAW76485 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ο,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 12; 31pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bufe A, Cromwell O,
Mueller W, Schramm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.8%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97DE-1013001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97DE-1013001.
                                                                                                                                                                                                                                                                                                                                                                                                                                        11-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                   Query Match
Best Local Similarity 66.7-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                                                                                     18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43 IIAGTPEVHAVK 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-522170/45.
                                                                                                                                                                                                                                                     7 VPKLDEVYNAAY
                                                                                                                                                                                                                                                                                     1 vpkldaaysvay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DE19713001-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Becker W,
                                                                                                                                                                                                                                                                                                                                                                                                     AAW76485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kahlert
                                                                                                                                                                                                                                                                                                                                     13
                                                                                                                                                                                                                                                                                                                                                      AAW76485
                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                    ò
     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ij
                                                                                                                                                                                  These
                                                                                                                                                                               sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                               Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW76449-W76534 are peptide fragments of a natural pollen allergen,
Phl p 5b; isolated from Graminae species. This allergen can be modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pollen; allergen; Phl p 5b; IgE; antibody; grass; reactivity; T cell; epitope; immunotherapy; allergy; hyposensitisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                   present invention provides a number of nucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    recombinant allergens - useful for immuno-therapy of
                                                                                                                                   Claim 17; SEQ ID NO: 6796; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pollen allergen Phl p 5b peptide fragment #25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jaeger L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ||| ||: | | :: | || || 2 nlvdhadpensgegragvmlngtlkgtdmdiitagdpdvvav 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 NAADHAAPEDKYEA-----FVLHFSEALHIIAGTPEVHAV 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44.5; DB 22;
Pred. No. 1.4e+02;
1; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fiebig H, Stuewe H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 12; 31pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bufe A, Cromwell O,
Mueller W, Schramm G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW76473 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.0%;
35.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97DE-1013001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97DE-1013001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Conservative
                                                                                                                                                                                                                                                                                                                                                                   European Patent Office
WPI; 2001-376931/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-522170/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    53 AA;
                  N-PSDB; AAH68261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DE19713001-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kahlert H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Becker W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Graminae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW76473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Graminae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     අ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

ö

Gaps

ö

Indels

5

```
Search completed: July 11, 2002, 10:55:51 Job time: 219.sec
                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                           Lol pV, is a major allergen of ryegrass pollen, and is encoded by the CDNA sequence of clone 12R (AAQ85932), a full-length clone derived from a lambda gtll library. Peptides (AAR71508-61) comprising at least one T cell epitope derived from the Lol pV protein are claimed, and can be used to treat or diagnose sensitivity to ryegrass pollen in an individual or to pollen proteins that are immunologically related to Lol pV, such as Dac gV (see AAR71507).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Functional surrogate; analyte; affinity receptor; immunoreactive group; mimic; homogenous immunoassay; detection; diagnostic analyte; Chlamydia; cardiac marker; tumour marker; allergen; hormone; fertility; myoglobin; pregnancy; infectious disease; ferritin; myosin light chain; troponin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                  Lolium perenne Lol pV and Dactylis glomerata Dac gV epitope(s) and DNA - for treating sensitivity to rye-grass pollen allergen or an immunologically cross-reactive allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                          Lolium perenne; Lol pV; Dactylis glomerata; Dac gV; epitope; sensitivity; ryegrass pollen allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44; DB 16; Length 20; Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FC22, from R26 library.
                                                                                                                       LPIX-8, peptide fragment of Lol pV protein allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                           AAR71515 standard; Protein; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW10845 standard; peptide; 29 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAb anti-HBsAg binder sequence,
                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 2; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.8%;
72.7%;
                                                                                                                                                                                                                                                                          (IMMU-) IMMULOGIC PHARM CORP
                                                                                                                                                                                                                                   94WO-US09024.
                                                                                                                                                                                                                                                      93US-0106016.
                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Conservative
                                                                                                                                                                                                                                                                                            Griffith IJ, Kuo M,
WPI; 1995-115444/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SKAPQLVPKLD 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match |
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :||| |:||||
8 akapglipkld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 AA;
                                                                                                                                                                        Lolium perenne.
                                                                                                                                                                                                                                   05-AUG-1994;
                                                                                                                                                                                                                                                      13-AUG-1993;
                                                                                                   02-NOV-1995
                                                                                                                                                                                           WO9506728-A
                                                                                                                                                                                                               09-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-NOV-1997
                                                                               AAR71515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW10845;
                                         RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                   AAR71515
            a
                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         surrogate is capable of competing effectively with the analyte for a limiting amount of an affinity receptor for the analyte. The conjugate exhibits an activity that is altered upon interaction with the affinity receptor and this activity to a be mead upon interaction with the affinity the analyte present in a sample. Functional surrogates such as this and with the analyte for a limiting amount of its affinity receptor. Functional surrogate to compete effectively and with the analyte for a limiting amount of its affinity receptor. They can be labelled for use in standard competitive affinity assays (esp. homogenous immunoassays) for detecting large macromolecules such as polypeptides, polysaccharides, polynucleotides, altocoproteins and lipid-containing macromolecules, as well as small haptens. Typical diagnostic analytes for detection include cardiac or tumour markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             allergens, hormones related to fertility-pregnancy or analytes associated with infectious disease. In particular, the assays are useful for detecting ferritin, follicle stimulating hormone, human growth hormone, immunoalobulin E, prolactin, parathyroid hormone, human placental lactogen, hepatitis antigens or antibodies against them, human chorionic gonadotropin, human luteinising hormone, cytomegalovirus, chlamydia, Streptococcus a, rubella, toxoplasma, herpes virus, DK-MB, myoslobin, myosin light chain, troponin, carcinoembryonic antigen, alpha-fetoprotein, prostate-specific antigen and CA125 (a tumour marker).
follicle stimulating hormone; human; growth hormone; immunoglobulin E; prolactin; parathyroid hormone; placental lactogen; hepatitis antigen; antibody; chorionic gonadotropin; luteinising hormone; cytomagalovirus; Streptococcus; rubella; toxoplasma; DK-MB; prostate-specific antigen; carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a monoclonal anti-hepatitis B antigen binder sequence from the R26 library which may be used in the conjugate of th invention. The novel labelled conjugate comprises at least one label attached to a functional surrogate of an analyte of interest. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Labelled functional surrogate of an analyte - useful as competitor molecule in affinity assays, esp. for detecting large macromolecules such as ferritin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.8%; Score 44; DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 78; ; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 51; Page 95; 156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .,
,,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95US-0476375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 KLDEVYNAAYNAADHAAPEDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::| |: |:||| | |:
3 eidpfyhpiysaadggarsde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 38.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carter JM, Lee-Own FV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CYTO-) CYTOGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-077284/07
                                                                                                                                                                                                                                                                                                                                                  W09641172-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                       19-DEC-1996.
```

```
1: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
4: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
5: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
6: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
6: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
7: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
8: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
9: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:*
110: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:*
113: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
114: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
115: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
116: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
117: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
118: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
119: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
110: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
1117: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
118: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
119: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
119: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
110: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
110: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
1117: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
1118: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
1119: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
                                                                                                                                                                                                                                              July 11, 2002, 10:50:47; Search time 29.69 Seconds (without alignments) 299.289 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ADKYKTFEAAFTVSSKRNLA.....SEALHIIAGTPEVHAVKPGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   434996
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                              US-09-696-169A-18
409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A_Geneseq_032802:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length: 0
Iength: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database
                                                                                                                                                                                                                                                                Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Score

Result Š

	Description	Phleum sp. allerge	Phleum sp. allerge	Kentucky Blue Gras	LPIX-10, peptide f	α	LPIX-6, peptide fr	LPIX-11, peptide f	Graminae pollen al	LPIX-12, peptide f	LPIX-8, peptide fr	Graminae pollen al
	DB ID	20 AAY25638	20 AAY25637	17 AAR89393	16 AAR71517	16 AAR71516	16 AAR71513	16 AAR71518	19 AAW76465	16 AAR71519	16 AAR71515	19 AAW76466
	Watch Length DB	80	57	20	20	20	20	20	12	20	20	12
% Query	Match	100.0	72.6	17.1	15.9	15.2	14.4	13.7	13.2	13.2	12.7	12.5

4 5 7 7 8 8 9 11 11

WPI; 1999-458255/38

					•
Novel human diagno Copolymer block pr Kentucky Blue Gras Copolymer molecula Propionibacterium	Copolymer block pr LPIX-13, peptide f Graminae polien al Kentucky Blue Gras Human secreted pro Novel human diagno	Human secreted pro Human secreted pro Copolymer molecula Kentucky Blue Gras Human 5' EST secre	מונוחות	Arabidopsis thalia Arabidopsis thalia Graminae pollen al Peptide #4724 enco Peptide #4831 enco Protein #4614 enco	Human brain expres Human bone marrow Peptide #4724 enco Peptide #4815 enco Peptide #4815 enco
ABG06223 AAB10561 AAR89392 AAY82573 AAU46409	AAB10562 AAR71520 AAW76464 AAR89391 AAB08919 ABG00995	AAB08978 AAB08979 AAY82574 AAR89387 AAY11961	AAU53006 AAU53006 ABB66772 AAG02471 AAU64369 AAY10914 AAG12165	AAG20982 AAG46642 AAW76471 ABB32073 ABB37325 ABB37325	AAM58018 AAM70455 AAM18290 AAM30778 AAM05901
22 21 21 22 22	21 21 22 23	27 27 20 20 20	1021222	2222	22222
			551 69 69		
CC 25 9	020107	rr9791	0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	004666	വവവവവ
12.3 12.1 12.0 11.9		iiiiii;		ннннн	::::::::::::::::::::::::::::::::::::::
0.4 88	. 4 4 4 4 4	46.94	4 4 4	4 4 4 4	44444
-14 44	*	7	444	4.4	
11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	17 18 19 21 22	22 2 2 3 3 4 3 3 4 3 3 5 5 5 5 5 5 5 5 5 5 5 5	330 0 0 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	35, 33, 38, 40,	4 4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5

## ALIGNMENTS

AAY25638

```
Major histocompatibility complex; class II; desensitising; human; allergen; grass; tree; weed; pollen; fungi; mould; food; insect; sting; chiromidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee; screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat; cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig; mice; gerbil; vaccine; treatment; prevention; hypersensitivity.
                                                                           Phleum sp. allergen Phl p 6 protein fragment #3
                                                                                                                                                                                                                                                                                                                                            (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
AAY25638 standard; protein; 80 AA
                                                                                                                                                                                                                                                                                                     98GB-0020474.
                                                                                                                                                                                                                                                                             99WO-GB00080
                                                  30-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                       Larche M;
                                                                                                                                                                                                                       W09934826-A1.
                                                                                                                                                                                                                                                                                                      21-SEP-1998;
09-JAN-1998;
                                                                                                                                                                                                                                                                            11-JAN-1999;
                                                                                                                                                                                                                                                  15-JUL-1999
                                                                                                                                                                                            Phleum sp
                         AAY25638;
                                                                                                                                                                                                                                                                                                                                                                       Kay AB,
```

```
Example 6; Page 65; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Poa pratensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9603106-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mohapatra SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-FEB-1996.
                                                                                                                                                                                                                                    Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                AAR89393;
                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                          AAR89393
                                                                                                                                                                                                                                                                                                                                                                                 RESULT
  ò
                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel method of desensitizing a patient to a polypeptide allergen and comprises administering to the patient a peptide derived from the allergen where restriction to a MHC Class II molecule cossessed by the patient can be demonstrated for the peptide and the peptide is able to induce a late phase response in an individual who possesses the MHC class II molecule. The methods can be used for desensitising patients to allergens present in e.g. grass, tree and weed including ragweed) pollens, fungl and moulds, foods, stinging insects, the chiromidae (non-biting midges), spiders and mites, housefly, fruit fly, sheep blow fly, screw worm fly, grain weed, silkworm, honeybee, non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of Tenibrio molitor beetle, mammals such as cat, dog, horse, cow, pig, Tenibrio molitor beetle, mammals such as cat, dog, horse, cow, pig, produce immunological vaccines which may be used to prevent and/or treat conditions involving hypersensitivity to allergens. This sequence
                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Major histocompatibility complex; class II; desensitising; human; allergen; grass; tree; weed; pollen; fungi; mould; food; insect; sting; chiromidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybbee; screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat; cockroach; beetle; dog; horse; cow; plg; sheep; rabbit; rat; guinea plg; mice; gerbil; vaccine; treatment; prevention; hypersensitivity.
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                            1 ADKYKTFEAAFTVSSKRNLADAVSKAPQLVPKLDEVYNAAYNAADHAAPEDKYEAFVLHF 60
                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                               80;
                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                            100.0%; Score 409; DB 20;
100.0%; Pred. No. 1.3e-42;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phleum sp. allergen Phl p 6 protein fragment #2.
 Desensitizing patients to polypeptide allergens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Desensitizing patients to polypeptide allergens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
                     Example 6; Page 65-66; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY25637 standard; protein; 57 AA.
                                                                                                                                                                                                                                                                                                                                                                                           61 SEALHIIAGTPEVHAVKPGA 80
                                                                                                                                                                                                                                                                                                                                                                                                         99WO-GB00080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98GB-0020474
98GB-0000445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                     80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI*: 1999-458255/38
                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Larche M;
                                                                                                                                                                                                                                                          80 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9934826-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phleum sp.
                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY25637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kay AB,
                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY25637
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
ò
                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                 a
```

```
This invention describes a novel method of desensitizing a patient to a polypeptide allergen and comprises administering to the patient a peptide derived from the allergen where restriction to a MtC class II molecule cossessed by the patient can be demonstrated for the peptide and the possesses the MtC class II molecule. The methods can be used for desensitising patients to allergens present in e.g. grass, tree and weed (including ragweed) pollens, fungi and moulds, foods, stinging insects, the chiromidae (non-biting midges), spiders and mites, housefly, fruit fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee, non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of the chiromidae control of the chiromidae of the mould of the chiromidae of the conditions involving hypersensitivity challengens. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide including at least 1 human antigenic determinant of Kentucky Blue Grass allergen - from Poa p IX 9p. of grass pollen allergens, used to desensities allergic individuals, prevent grass pollen allergy and deplete allergen-specific antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present peptide is a human antigenic determinant contg. peptide, comprising residues 129–148 of the recombinant Kentucky Blue Grass pollen allergen rKBG60, which is from the Poa p IX gp. of grass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigenic determinant; recombinant; Kentucky Blue Grass; pollen; allergen: antigenic; rKBG60; Poa p IX group; desensitisation; allergy; prevention; development; reaction; grass; antibody; anergise; producting cell; diagnosis; human; clone 60; immunological response; B-cell; hIgG; hIgE; T-cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 SKAPQLVPKLDEVYNAAYNAADHAAPEDKYEAFVLHFSEALHIIAGTPEVHAVKPGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kentucky Blue Grass pollen allergen rKBG60 resides 129-148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           represents a Phleum sp. (Timothy grass) Phl p 6 allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.6%; Score 297; DB 20;
100.0%; Pred. No. 4.6e-29;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 5; Page 29; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR89393 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95WO-CA00439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94US-0280455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYMA-) UNIV MANITOBA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-116753/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity
Matches 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 AA;
```

us-09-696-169a-18.closed.rag

Ä.

Ŋ

(first entry)

20

```
Lolium perenne Lol pV and Dactylis glomerata Dac gV epitope(s) and DNA - for treating sensitivity to rye-grass pollen allergen or an immunologically cross-reactive allergen.
                                                                                                                                                                                Lolium perenne; Lol pV; Dactylis glomerata; Dac gV; epitope; sensitivity; ryegrass pollen allergen.
                                                                                                                                                     LPIX-9, peptide fragment of Lol pV protein allergen.
                                                                       AAR71516 standard; Protein; 20
                                                                                                                                                                                                                                                                                                                                                          (IMMU-) IMMULOGIC PHARM CORP.
      1 ydvaykaaegatpeakydaf
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-115444/15.
                                                                                                                                                                                                                       Lolium perenne.
                                                                                                                                                                                                                                                                                                     05-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                    Griffith IJ,
                                                                                                                          02-NOV-1995
                                                                                                                                                                                                                                                                                                                               13-AUG-1993;
                                                                                                                                                                                                                                                WO9506728-A.
                                                                                                                                                                                                                                                                            09-MAR-1995.
                                                                                                 AAR71516;
                                                         AAR71516
                                              RESULT
                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lol pV, is a major allergen of ryegrass pollen, and is encoded by the CDNA sequence of clone 12R (AAQ85932), a full-length clone derived from a lambda gtll library. Peptides (AAR71508-61) comprising at least one T cell epitope derived from the Lol pV protein are claimed, and can be used to treat or diagnose sensitivity to ryegrass pollen in an individual or to pollen proteins that are immunologically related to Lol pV, such as Dac gV (see AAR71507).
pollen allergens. A compsn. comprising the peptide and a carrier can be used to desensitise allergic individuals, and prevent allergic individuals from developing an allergic reaction to grass pollen. The compsn. may also be used to deplete allergen specific antibodies from an individual, and anergise allergen specific antibody producing cells. The peptide can be used to diagnose grass pollen allergy, and has the following human immunological response profile, B-cell (hIgG (-)/hIgE (-)), T-cell (-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lollum perenne Lol pV and Dactylis glomerata Dac gV epitope(s) and DNA - for treating sensitivity to rye-grass pollen allergen or an immunologically cross-reactive allergen.
                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                          pV; Dactylis glomerata; Dac gV; epitope;
                                                                                                                                                                  DB 17; Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 16; Length 20
                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                              LPIX-10, peptide fragment of Lol pV protein allergen.
                                                                                                                                                                                            3;
                                                                                                                                                                Score 70; DB 17
Pred. No. 0.085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.9%; Score 65; DB 1660.0%; Pred. No. 0.35;
                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     sensitivity; ryegrass pollen allergen
                                                                                                                                                                                                                                                                                                                   ¥.
                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Luqman M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 2; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IMMU-) IMMULOGIC PHARM CORP
                                                                                                                                                                17.1%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93US-0106016.
                                                                                                                                                                                                                                                                                                                AAR71517 standard; Protein;
                                                                                                                                                                                                                                   61 SEALHIIAGTPEVHAVKP 78
                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kuo M,
                                                                                                                                                                                                                                                                                                                                                                                                                         Lolium perenne; Lol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-115444/15.
                                                                                                                                                               Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                         20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lolium perenne.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Griffith 1J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                    02-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9506728-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-MAR-1995
                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                                                         AAR71517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
    88888888888
                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                    ò
```

Luqman M;

Kuo M,

93US-0106016 94WO-US09024

```
ö
                         Lol pV, is a major allergen of ryegrass pollen, and is encoded by the cDNA sequence of clone 12R (AAQ85912), a full-length clone derived from a lambda gtll library. Peptides (AAR71508-61) comprising at least one T cell epitope derived from the Lol pV protein are claimed, and can be used to treat or diagnose sensitivity to ryegrass pollen in an individual or to pollen proteins that are immunologically related to Lol pV, such as Dac gV (see AAR71507).
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lolium perenne; Lol pv; Dactylis glomerata; Dac gV; epitope; sensitivity; ryegrass pollen allergen.
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPIX-6, peptide fragment of Lol pV protein allergen.
                                                                                                                                                                                                                                                               .
S
                                                                                                                                                                                                                             DB 16;
                                                                                                                                                                                                                                                 0.81;
                                                                                                                                                                                                                                               Pred. No. 0.81
; Mismatches
                                                                                                                                                                                                                               Score 62;
                                                                                                                                                                                                                                                                                                                                                                                                                         AAR71513 standard; Protein; 20 AA.
Claim 1; Fig 2; 110pp; English.
                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                           15.2%;
57.9%;
                                                                                                                                                                                                                                                                                                  27 PQLVPKLDEVYNAAYNAAD 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                    | |:|||| |: || ||:
| pglipkldtaydvaykaae
                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                           20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lolium perenne.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-NOV-1995
                                                                                                                                                                                                                                                               11;
                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR71513;
                                                                                                                                                                                                                                                                 Matches
```

ó

Gaps

ö

Indels

5;

3; Mismatches

26

37 YNAAYNAADHAAPEDKYEAF

ò

12; Conservative

Best Local Similarity

Matches

Gaps

ö

Indels

. 9

Length 20;

```
Lol pV, is a major allergen of ryegrass pollen, and is encoded by the cDNA sequence of clone 12R (AAQ85932), a full-length clone derived from a lambda gtll library. Peptides (AAR71508-61) comprising at least one re call pricope derived from the Lol pV protein are claimed, and can be used to treat or diagnose sensitivity to ryegrass pollen in an individual or to pollen proteins that are immunologically related to Lol pV, such as Dac gV (see AAR71507).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phl p 5b, isolated from Graminae species. This allefgen can be modified and the reactivity of the modified allergens with IgE antibodies to grass pollen allergens is reduced or eliminated while their reactivity with T cells is retained. The genes for the allergens are modified so that the encoded polypeptides have one or more amino acid substitutions, deletions and/or additions. The dominant T-cell epitopes of the allergens are not genetically altered. Such allergens have applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pollen; allergen; Phl p 5b; IgE; antibody; grass; reactivity; T cell; epitope; immunotherapy; allergy; hyposensitisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW76449-W76534 are peptide fragments of a natural pollen allergen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified recombinant allergens - useful for immuno-therapy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 19; Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in the immunotherapy of allergies e.g. hyposensitisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Graminae pollen allergen Phl p 5b peptide fragment #17.
                                                                                                                                                                                                                                                                                                DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 54; DB 1
Pred. No. 4;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fiebig H,
                                                                                                                                                                                                                                                                                                Score 56;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bufe A, Cromwell O, F
Mueller W, Schramm G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW76465 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 12; 31pp; German.
  Claim 1; Fig 2; 110pp; English.
                                                                                                                                                                                                                                                                                                                                             ٠.
ښ
                                                                                                                                                                                                                                                                                                13.7%;
                                                                                                                                                                                                                                                                                                                                                                                          99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.2%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 atpeakydafvtaltealrv 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97DE-1013001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                          47 AAPEDKYEAFVLHFSEALHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 13.2
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
'-haq 11; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-522170/45.
                                                                                                                                                                                                                              20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DE19713001-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Becker W,
Kahlert H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW76465;
                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Graminae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW76465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME OF COLOR OF STREET OF
    8 X C C C C C C C X 8
                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lol pV, is a major allergen of ryegrass pollen, and is encoded by the CDNA sequence of clone 12R (AAQ85932), a full-length clone derived from a lambda gill library. Peptides (AAR71508-61) comprising at least one T cell epitope derived from the Lol pV protein are claimed, and can be used to treat or diagnose sensitivity to ryegrass pollen in an individual or to pollen proteins that are immunologically related to Lol pV, such as Dac gV (see AAR71507).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                   Lolium perenne Lol pV and Dactylis glomerata Dac gV epitope(s) and DNA - for treating sensitivity to rye-grass pollen allergen or an immunologically cross-reactive allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LoTium perenne Lol pV and Dactylis glomerata Dac gV epitope(s) and DNA - for treating sensitivity to rye-grass pollen allergen or an immunologically cross-reactive allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lolium perenne; Lol pV; Dactylis glomerata; Dac gV; epitope; sensitivity; ryegrass pollen allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 59; DB 16; Length 20;
Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPIX-11, peptide fragment of Lol pV protein allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR71518 standard; Protein; 20 AA.
                                                                                                                                                                                                                              Kuo M, Lugman M;
                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 2; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lugman M;
                                                                                                                                                                                 (IMMU-) IMMULOGIC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.48;
75.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IMMU-) IMMULOGIC PHARM CORP
                                                                                                                                    93US-0106016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93US-0106016
                                                                                         94WO-US09024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ADKYKTFEAAFTVSSK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||:| |||||: ||||
5 adkfkifeaafsessk 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kuo M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-115444/15.
                                                                                                                                                                                                                                                                        WPI; 1995-115444/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lolium perenne.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Griffith IJ,
                                                                                                                                                                                                                              Griffith IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-NOV-1995
                                                                                         05-AUG-1994;
                                                                                                                                    13-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09506728-A.
W09506728-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-MAR-1995
                                            09-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR71518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR71518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
```

ü

ö

Gaps

;

0; Indels

```
Lolium perenne Lol pV and Dactylis glomerata Dac gV epitope(s) and DNA - for treating sensitivity to rye-grass pollen allergen or an immunologically cross-reactive allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 2; 110pp; English.
                                                                                                                                                                                                                                                                                      (IMMU-) IMMULOGIC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.7%;
62.5%;
                                                                                                                                                                                                                                     93US-0106016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97DE-1013001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97DE-1013001.
                                                                                                                                                                                 94WO-US09024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               || : :||| |:||||
3 latsaakapglipkld 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 LADAVSKAPQLVPKLD
                                                                                                                                                                                                                                                                                                                                          Kuo M,
                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-115444/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-522170/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 10; Conserv
                        Lolium perenne.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DE19713001-A1
                                                                                                                                                                                                                                                                                                                                       Griffith 1J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-MAR-1997;
                                                                                                                                                                              05-AUG-1994;
                                                                                                                                                                                                                                     13-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-DEC-1998
                                                                         WO9506728-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Becker W,
Kahlert H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW76466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Graminae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW76466
ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE STATE OF THE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lol pV, is a major allergen of ryegrass pollen, and is encoded by the CDNA sequence of clone 12R (AAQ85932), a full-length clone derived from a lambda gtil library. Peptides (AAR71508-61) comprising at least one T cell epitope derived from the Lol pV protein are claimed, and can be used to treat or diagnose sensitivity to ryegrass pollen in an individual or to pollen proteins that are immunologically related to Lol pV, such as Dac gV (see AAR71507).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lolium perenne Lol pV and Dactylis glomerata Dac gV epitope(s) and DNA - for treating sensitivity to rye-grass pollen allergen or an immunologically cross-reactive allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                            Lolium perenne; Lol pV; Dactylis glomerata; Dac gV; epitope; sensitivity; ryegrass pollen allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lolium perenne; Lol pV; Dactylis glomerata; Dac gV; epitope; sensitivity; ryegrass pollen allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Indels
                                                                                                                                                                                                                                                                                                                                                             LPIX-12, peptide fragment of Lol pV protein allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPIX-8, peptide fragment of Lol pV protein allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 16;
7.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.2%; Score 54; DB 60.0%; Pred. No. 7.8; Live 2; Mismatches
                                                                                                                                                                                                       AAR71519 standard; Protein; 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR71515 standard; Protein; 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 2; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IMMU-) IMMULOGIC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 VLHFSEALHIIAGTPEVHAV 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | :||| :||| ||||||
| vtaltealrviagalevhav 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94WO-US09024.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93US-0106016.
                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 13.2
Best Local Similarity 60.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Griffith IJ, Kuo M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-115444/15.
                                                 ||:||||||||
| dkfktfeaaft 11
                   DKYKTFEAAFT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lolium perenne.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-AUG-1993;
                                                                                                                                                                                                                                                                                                            02-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9506728-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR71515;
                                                                                                                                                                                                                                                           AAR71519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
                     N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR71515
                                                                                                                                                   RESULT
```

ö

```
Lol pV, is a major allergen of ryegrass pollen, and is encoded by the CDNA sequence of clone 12R (AAQ85932), a full-length clone derived from a lambda gt11 library. Peptides (AAR71508-61) comprising at least one used to treat or diagnose sensitivity to ryegrass pollen in an individual or to pollen proteins that are immunologically related to Lol pV, such as Dac gV (see AAR71507).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pollen; allergen; Phl p 5b; IgE; antibody; grass; reactivity; T cell; epitope; immunotherapy; allergy; hyposensitisation.
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                          Length 20;
                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Graminae pollen allergen Phl p 5b peptide fragment #18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jaeger L;
                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fiebig H, ,
                                                                                                                                                                                                                                                                                                       core 52; DB 1
red. No. 14;
Mismatches
                                                                                                                                                                                                                                                                                                       Score 52;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bufe A, Cromwell O, F
Mueller W, Schramm G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW76466 standard; peptide; 12 AA.
```

ò 셤 

```
15-DEC-2000 (first entry)
                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McGrath KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-542235/49.
                                                                                                                                                                                                                          Best_Local Similarity
Matches 13; Conserv
                                                                                                                                                                           76 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US6090911-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUL-2000.
                                                                                                                                                                                                                                                                                                                                                                         AAB10561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Petka WA,
                                                                                                                                                                           Sequence
                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                           13
                                                                                                                                                                                                                                                                                                                                      AAB10561
                                                                                                                                                                                                                                                                                                                           RESULT
 δ
                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (IL) is useful in for generating antibodies against it, detecting or
                                                                     phl p 5b, isolated from Graminae species. This allegen can be modified and the reactivity of the modified allergens with IgE antibodies to grass pollen allergens is reduced or eliminated while their reactivity with T cells is retained. The genes for the allergens are modified so that the encoded polypeptides have one or more amino acid substitutions, that the encoded polypeptides have one or more amino acid substitutions, allergens and/or additions. The dominant T-cell epitopes of the allergens are not genetically altered. Such allergens have applications in the immunotherapy of allergies e.g. hyposensitisation.
                                                                                                                                                                                                                                                    Gaps
                                                             AAW76449-W76534 are peptide fragments of a natural pollen allergen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                  ö
Modified recombinant allergens - useful for immuno-therapy of
                                                                                                                                                                                                                          DB 19; Length 12;
                                                                                                                                                                                                                Score 51; DB 1
                                                                                                                                                                                                                                    Pred. No. 9.4;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID No 36582; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human diagnostic protein #6214
                                                                                                                                                                                                                                                                                                                                                            ABG06223 standard; Protein; 76 AA.
                                    Example 1; Page 12; 31pp; German.
                                                                                                                                                                                                                          12.5%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                            13-FEB-2002 (first entry)
                                                                                                                                                                                                                         Query Match 12.5
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                      5 KTFEAAFTVSSK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                       12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAS70410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-0CT-2001
             allergies
                                                                                                                                                                                                                                                                                                                                                                                    ABG06223;
                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human;
                                                                                                                                                                                                                                                                                                                                     RESULT 12
                                                                                                                                                                                                                                                                                                                                                ABG06223
 ò
                                                                                                                                                                                                                                                                                                g
```

```
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel synthetic block copolymer XYZ comprising two alpha-helical protein blocks X and Z, a water soluble, random-coil protein block Y which links X and Z, and linker proteins for linking the alpha-helical protein blocks to the random-coil protein block. The products of the invention have vulnerary activity. A copolymer produced from a gene that encodes a derivative of AC_1_0A copolymer was suspended in water to form a gel, which was then used to treat a wound. The cell binding domain was the integrin ArgGlyAspSer sequence which is known to bind to gplia/IIIa proteins expressed on fibroblast cells necessary for matrix formation for the regeneration of skin. Fibroblasts become
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coiled coil protein; copolymer blocker; vulnerary; wound treatment; integrin; fibroblast cell; matrix formation; skin regeneration; scaffold; antibiotic; dressing; abrasion; burn.
quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of Sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dressing abrasion, burn or non-puncture wound, comprises two alpha-helical protein blocks, random-coil protein block and linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic block copolymer with an antibiotic compound, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 50.5; DB 22;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 VSKAP---QLVPKLDEVYNAAYNAADHAAPEDKYEAFV 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Column 33-34; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copolymer block protein insert L2-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tirrell DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB10561 standard; protein; 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0956307.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                970S-0956307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYMA-) UNIV MASSACHUSETTS.
```

```
;
           serving as a scafed for the regeneration of tissue surrounding the wound. A synthetic block copolymer together with an antibictic compound is useful for wound dressing. The copolymer is useful for dressing abrasion, burn or non-puncture wound. Unlike conventional polymers, the polymers of equal size are produced biologically from a single template. The intermolecular binding of alpha-helical blocks are monodisperse which gives a uniform pore size depending on the length of random-coil block. The new copolymers have low molecular weight hence have decreased viscosity solutions or gals under suitable conditions. This sequence method of the invention.
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide including at least 1 human antigenic determinant of Kentucky Blue Grass allergen - from Poa p IX gp. of grass pollen allergens, used to desensitise allergic individuals, prevent grass pollen allergy and deplete allergen-specific antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present peptide is a human antigenic determinant contg. peptide, comprising residues 109-128 of the recombinant Kentucky Blue Grass pollan allergen KR6660, which is from the Poa p IX sp. of grass pollen allergens. A compson. comprising the peptide and a carrier can be used to desensitise allergic individuals, and prevent allergic individuals from developing an allergic reaction to grass pollen. The compson may also be used to deplete allergen specific antibodies from an individual, and anergise allergen specific antibodies from an individual, and anergise allergen specific antibody producing cells. The peptide can be used to diagnose grass
 entrapped within the gel and thus remain at the site of the wound,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antigenic determinant; recombinant; Kentucky Blue Grass; pollen; allergen; antigenic; rKBG60; Poa p IX group; desensitisation; allergic; allergy; prevention; development; reaction; grass; antibody; anergise; producing cell; diagnosis; human; clone 60; immunological response; B-cell; hIgG; hIgE; T-cell.
                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                   Length 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kentucky Blue Grass pollen allergen rKBG60 resides 109-128.
                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                     21;
                                                                                                                                                                                                                                                                                                 Score 49.5; DB 21
Pred. No. 1.5e+02;
7; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                   17 RNLADAVSKAPQLVPKL-DEVYNAAYNAADHAAPED 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR89392 standard; peptide; 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; Page 29; 59pp; English.
                                                                                                                                                                                                                                                                                                     12.1%;
33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94US-0280455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95WO-CA00439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 33.3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYMA-) UNIV MANITOBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-116753/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Poa pratensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mohapatra SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9603106-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-FEB-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR89392;
                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR89392
8888888888888
                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ΟŻ
```

```
AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention according to molecular invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of an an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for allatiramer acctate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune opophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, crohn's disease, chronic immune thrombocytopaenia curpura, colitis, contact sensitivity disease, diabetes mellitus, Graves
                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glatizamer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antipporiatic; dermatory; antidaemter; thyromimette; haemostatic; antipporiatic; dermatological; antianaemter; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Pashinoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                         Gaps
pollen allergy, and has the following human immunological response profile, B-cell (hIgG (-)/hIgE (-)), T-cell (+).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copolymer molecular weight TV-marker amino acid sequence SEQ ID
                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copolymer; molecular weight marker; TV-marker; immune disease;
                                                                                                                 Length 20;
                                                                                                                                                         Indels
                                                                                                                                                       2
                                                                                                                   17;
                                                                                                                 Score 49; DB
Pred. No. 32;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 10; Page 14; 72pp; English
                                                                                                                                                                                                                                                                                                                                 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTD.
                                                                                                                 12.0%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US22402.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0101693.
                                                                                                                                                                                                                                                                                                                               AAY82573 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (YEDA ) YEDA RES 6 DEV CO L'
(TEVA-) TEVA PHARM USA INC.
                                                                                                                                                                                                                  | | :|: | || ||: :|
| ayksaegatpeakyddyv 18
                                                                                                                                                                                            40 AYNAADHAAPEDKYEAFV 57
                                                                                                                                                                                                                                                                                                                                                                                                            28-JUL-2000 (first entry)
                                                                                                                                                       9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-317499/27.
                                                                                                                 Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200018794-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
                                                        20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gad A, Lis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-APR-2000
                                                                                                                                                                                                                                                                                                                                                                      AAY82573;
                                                            Seguence
                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                         RESULT 1
                                                                                                                                                                                                                                                                                                                                   SSXS
                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                            g
```

Search completed: July 11, 2002, 10:51:26 Job time: 39 sec